

OM protein - protein search, using SWISSPROT
Run on: April 23, 2003, 10:58:30 ; Search time 15.0943 Seconds
(without alignments)
1617.710 Million cell updates/sec

```
Title: 1326
Perfect score:
Sequence: 1 MPAKTPILYKANNKKGKE.....QLDGPSSLDLVE.....
```

Searched: 283224 seqs, 961344000
Chosen parameters: 283224

Maximum	match	100
Listing	first	45 summaries

```
PIR_73:*
1:  p1r1:*
2:  p1r2:*
3:  p1r3:*
4:  p1r4:*
```

SUMMARIES

Description
hypothetical protein MSE5
serum protein comp1
nuclear pore compl
coagulation factor
phorbium receptor
hypothetical prote
hypothetical prote
transcription fact
frequency clock pi
hypothetical prote
hypothetical prote
hypothetical prote
HIV-Ep2 enhancer-b
DNA-directed DNA P
hypothetical prote
hypothetical prote
transcriptional fac
hypothetical prote
hypothetical prote
evolved beta-D-gal
serine-rich protei
lysine-rich protei
Lys
Lacta protein - Li
probable RNA-dinl
probable collagen co
but emergence prote
probable glycolipid
TCOP1 protein - mo
DNA (cytosine 5-)

myogenesis protein
hypothetical prote
tensin - chicken
transposable MADS-box
transcription fact
fibrinogen-binding
tensin, cardiac mu
hypothetical prote
hypothetical prote
tensin - chicken (tensin)
hypothetical prote
hypothetical prote
hypothetical prote
ubiquitous TPR motif
K1AA0624 protein -
hypothetical prote

100

protein DKFZp434A0530.1 - human

hypolincrin
C:Species: Homo sapiens (man)
04-Feb-2000 # revc_...
#sequence_revision

C; Date: 04 Jan 2000
C; Accession: T46465
S: Mewes, H.W.; Cassenhuber, J.
January 2000

R; Blum, H.; Bacter
submitted to the Protein S
73303A

A; Reference number: T46465
Accession: T46465

A;Status: Preliminary
Molecule type: mRNA

A;Residues: 1-234
References: EMB

A; Experimental source.

A;Note: DKFZP434A0530..1

Query	Match	Similarity
1	1	1.0
2	1	1.0
3	1	1.0
4	1	1.0
5	1	1.0
6	1	1.0
7	1	1.0
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92	1	1.0
93	1	1.0
94	1	1.0
95	1	1.0
96	1	1.0
97	1	1.0
98	1	1.0
99	1	1.0
100	1	1.0

Best of 254; Consequence of 254; Matches 254;

1 МРАКТРИЦКАА
QY

1 ПРАКТИКАА

61 GNYELLPGNOEK

61 GNYELLPGNQEI

121 PLSPTYENSK

121 PLSPTVNSK

181 SSQGRDSSSS

181 SSGGRDSHSS

ST.J.DEVL.NVM

ST. DEVIL NUM 21

3

RESULT 2

AA2913
serum protein MSE55

C; Species:
C; Date: 04-Mar-1993

C; Accession: ...
R: Bahou, W. F.; Camp

J. Biol. Chem.	267
A: Title:	CDNA cloning

—

100

0Y	13	NNKGGKFLRDIISDPDSSPP	31:	Makmatches	76:	Indels	66:	Gaps
1B	25	SSSGGR-----RLTADWISHPGDRPHHIIKGGKQDNDYAGDSTL-----QCNTEYL	66					
2Y	67	PGN--OENAHIGOPPGHNEEFKFNSTSDSVTEPSPYKNIISLPTTGGSOALMLPILS	77					
3b	78	FNSTLAKTLQIVRVGAPRRRAPSPPAPSPAPISPIKNIISLPQ-----	124					
4Y	125	PVTNSKQSGCRGPAKIPRLSCPCPWEKAEKSSLENTGYHQDITSNSSGGSASOSG	184					
5b	126	-----NQAWISLVVGLKSTD						
6Y	185	RDISSSLE--GYPMWPMEDMFPTPCELINGKTKRSESLDLSGLSLDLDGPSSL	243					
7Y	156	LDGEGCTIIRLRSEKPRHNDRGSPSE--PGLRSPDLSL-----FRDLDGPSSL	207					
8Y	244	DELYANM	250					
9Y	208	SELLGYM	214					

[illegible]

RESULT 4
EZHU
coagulation factor VIII precursor [validated] - human

N.Alternate names: antithromphillc factor A; coagulation factor VIII; prococulant co
C.Species: Homo sapiens (man)
C.Date: 28-Aug-1985 #sequence
A.Accession: I54318; #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
R.Gitschler, J.; Wood, W.I.;
Hum. Mol. Genet. 1, 199-200, 1992
A.Title: Sequence of the exon containing regions of the human factor VIII gene.
A.Reference number: I54318; MUID:93265012; PMID:1303718
A.Accession: I54318
A>Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-1921, S', 1923-2351 <RES>
A.Cross-references: DBJ:M88648; NID:g182381; PIDN:AA52420.1; PID:g182383
Nature 312, 330-337, 1984
A>Title: Expression of active human factor VIII from recombinant DNA clones.
A.Reference number: A00525; MUID:85061548; PMID:6438526
A.Accession: A00525
A.Molecule type: mRNA
A.Residues: 1-2351 <MOO>
A.Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
S., D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A>Title: Molecular cloning of a cDNA encoding human antithromphillc factor.
A.Accession: I58059; MUID:85061550; PMID:6438528
A>Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-174, V', 16-1259, 'E', 1261-2351 <RES>
A.Cross-references: GB:M01740; NID:g182802; PIDN:AA52484.1; PID:g182803
.B.; Randolphi, A.; Blacher, R.; Burke, K.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; K
DNA 4, 333-339, 1985
A>Title: Characterization of the polypeptide composition of human factor VIII:C and t
A.Reference number: A23584; MUID:86081164; PMID:3935400
A.Accession: A23584
A.Molecule type: MRNA
A.Residues: 1-2351 <TRU>
R.Eaton, D.; Rodriguez, H.; Venhar, G.A.
Biochemistry 25, 505-512, 1986
A>Title: Proteolytic processing of human factor VIII. Correlation of specific cleavag
ity.
A.Reference number: A26174; MUID:86159740; PMID:3082357
A.Accession: A26174
A.Molecule type: Protein
A.Residues: 20-36, 392-399, 'X', 401-402, 1668-1678, 1709-1722, 'D', 1723-1725, 1741-1755 <EA
Biochemistry 31, 3315-3325, 1992
A>Title: Identification and functional importance of tyrosine sulfate residues within
A.Reference number: A42348; MUID:92207952; PMID:1554716
A.Accession: A42348
A.Molecule type: protein
A.Residues: 20-36, 356-371, 392-408, 582-594, 1668-1669, 'X', 1671, 1672-1692, 1693-1708, 1709
A.Experimental source: recombinant material from Chinese hamster ovary cells
R.Pipe, P.J.; Smudzyn, T.M.
J Biol. Chem. 264, 14005-14010, 1989
A>Title: Interubunit fluorescence energy transfer in human factor VIII.
A.Reference number: A43866; MUID:89340500; PMID:2503350
A.Accession: A43866
A.Molecule type: Protein
A.Residues: 'X', 517-523, 1853-1860, 'X', 1862-1864, 'X', 1866 <FA>
R.Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Hutner, W.B.; Verbeet, M.P.; Mettens,
A.Biol. Chem 266, 740-746, 1991
A>Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential f
A.Content: annotation; sulfation
R.Gitschler, J.; Wood, W.I.; Goralka, T.M.; Wilson, K.L.; Chen, E.Y.; Eaton, D.H.; Velha
Nature 312, 326-330, 1984
A>Title: Characterization of the human factor VIII gene.
A.Reference number: A56196; MUID:85061547; PMID:6438525

A:Title: Whole genome sequencing of melicillin-resistant *Staphylococcus aureus*.
 A:Accession: F90073
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2271 <RUP>
 A:Cross-references: GB:BA000018; PID:g13702612; PIDN:BA043752.1; GSPDB:GN00149
 A:Experimental source: strain N315
 A:Gene: SA2447

Query Match
 Best local similarity 7.3%; Score 97; DB 2; Length 2271;
 Matches 44; Conservative 16; Mismatches 66; Indels 36; Gaps 5;

QY 85 FRANSTDSVETFPSPYLKNAISLPTIGSOALMLPLSPYFNKQESFGPKLRLS 144
 DB 1274 FKSESVSTLSMST-STLSNSTSLST-----SLSDSTSDSKSDSLSTSM----- 1317
 QY 145 CEPVMEKAKQKSSLENGTVHOGDTSWSSGSSASQSGDSSSSLSSEQYDWPADMD 204
 DB 1318 --STSDSTLSYKSDSTSTSLSGSTSESESDSTSSSKSDSTSMISMS----- 1366
 QY 205 FDMPTPELTKG--KTKSEESLDTLGLSLQLDLGSLD 244
 DB 1367 -----QSTSGSTSTSTSLSDSTSLSSASNMQSGVD 1401

RESULT 7

T00530
 N:Alternative names: hypothetical protein At2g19100 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
 C:Accession: T00530; E84572
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandón, R.C.; Sykes, A.
 A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
 A:Reference number: Z14167
 A:Accession: T00530
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1447 <RUP>
 A:Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176712
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84572
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1447 <STO>
 A:Cross-references: GB:AE002093; NID:g3176712; PIDN:AA12028.1; GSPDB:GN00139
 A:Gene: AT2g19100; T20K24.11
 A:Map position: 2
 A:Introns: 268/3; 444/1; 988/2; 1037/1; 1105/1

Query Match
 Best local similarity 7.3%; Score 96.5; DB 2; Length 1447;
 Matches 42; Conservative 23; Mismatches 74; Indels 21; Gaps 5;

QY 31 ISPPIGDRRHITHIGEGDHFVGDIFLQNYELLPNQKRAHLGQFPGHNEFRANST 90
 DB 333 ITPPTGSGSPITKIGEL---KGEVSTLSNSTSVLSGDEDEVERGKTIKIPAGE---ETK 384
 QY 91 SDSVFTETPS---PVLKNAISLPTIGSOALMLPLSPYFNKQESFGA--KLPRLSC 145
 DB 385 KDPGTEVPYVKVTQSDHVAHRTVONQRLSLPRGSKTAHKVLSNSTFOSNRNPKDKK 444

QY 146 EPVMEKAKQKSSLENGTVHOGDTSWSSGSSASQSGR 185
 DB 445 TRVKEDKAKQVLSKLFN-----DMSMITNPEYNSGR 476

RESULT 8

S26706

transcription factor SWI3 - yeast (*Saccharomyces cerevisiae*)
 N:Alternative names: protein J0495; protein YJL176c; transcription factor TYZ2
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 21-Jul-2000
 C:Accession: S26706; S26832; S56959
 R:Peterson, C.L.; Herskowitz, I.
 A:Title: Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a glo
 Cell 69, 573-583, 1992
 A:Reference number: S26706; MUID:92154671; PMID:1339306
 A:Accession: S26706
 A:Molecule type: DNA
 A:Residues: 1-825 <PEP>
 A:Cross-references: EMBL:M84390; NID:g172799; PIDN:AA35136.1; PID:g172800
 R:Odenhuy, C.
 A:Reference number: S23890
 A:Accession: S23892
 A:Molecule type: DNA
 A:Residues: 1-825 <LOE>
 R:Odenhuy, C.; Piravandi, E.; Rinke, M.; Domdey, H.
 A:Reference number: S56937
 A:Accession: S56959
 A:Molecule type: DNA
 A:Residues: 1-825 <OEP>
 A:Cross-references: EMBL:Z49451; NID:g1008372; PID:g1008373; MIPS:YJL176C
 C:Gene: SGD:SWI3; TYR2
 A:Cross-references: SGD:S0003712; MIPS:YJL176C
 A:Map position: 10L
 C:Function:
 A:Description: transcription regulation
 C:Keywords: nucleus; transcription regulation

Query Match
 Best local similarity 7.2%; Score 96; DB 2; Length 825;
 Matches 50; Conservative 31; Mismatches 75; Indels 42; Gaps 9;

QY 69 NOEKALQGFQCHNEFRANSTDSVETFPSPYLKNAISLPTIGSOALMLPLSPV-T 127
 DB 88 SQETSTESRAQNVFQDNDSDNLFGETESSVSNANPISIP-----TNPVN 138
 QY 128 FNSK-----QESFGPKLRLSCFVMEKAKQKSSLENGTVHOGDTSWSSGSA 178
 DB 139 ENNRPAIKEDSTIDNSGDK-----NMEDYKLOKEEP-----ENNYIIR-----V 181
 QY 179 SOSQGRDSSSSLSQYDWPADMDFHP--TPCELKTKTSESLDGLSLSTQL 236
 DB 182 KEESQ-PDENTKMDVEED--DEDDQPMISPDNSIFEDTKSESKOLGNTSSVANPSS 237
 QY 237 DLGSLDEVLVMDKRNK 254
 DB 238 EIPDAKKAQEDIIKTE 255

RESULT 9

T42013

frequency clock protein - *Creopus spinulosus*
 C:Species: *Creopus spinulosus*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
 C:Accession: T42013
 R:Lewis, M.T.; Morgan, L.W.; Feldman, J.F.
 M.O. Gen. genet. 253, 401-414, 1997
 A:Title: Analysis of frequency (ftr) clock protein homologs: evidence for a helix-turn
 A:Reference number: Z22024; MUID:97188515; PMID:9037100

[illegible]

Best Local Similarity 21.7%; Pred. No. 4.8;
Matches 51; Conservative 26; Mismatches 107; Indels 51; Gaps 7;

OY 55 DIFLL-OGNVEL-LPNOEKALHGPCHNEFFRANS-----
Db 166 DYFFLRSDAEELPVKESLSRSGSFPSAYHFHEDNLYRFADVQARSQSLSPRKOS 225
OY 90 -----TSDVTEPSPVLYKNAISLPTIGSQALMLPLSPVTFNSKQSEFGPATL-----
Db 226 SGINGRTAHSHREKRPVANSANGHSRPSGSG-----NMHSRPSGSGSKMNS 140
OY 141 -PRLSCEPVEEKAQKESLLENGTVHOGDTWSSGSAQSOGGRDSSLSLSPQYDWM 274
Db 275 RPAISGSGOMPSRASSGSGOMSRAY-SGSGRPASSGSGOMSRNPAPASGSGOQOR 199
OY 200 PAEMEDHPPELIGKIKKESLSLDTGLSLSLQDLGLDGLDEVLYLVNDKMK 254
Db 334 PASSGSGORPAS-----SGSGRPASSGSGORPSTNQAPMRPGSGSTMGQSANR 384

RESULT 13

MMHUE2

HIV-EP2 enhancer-binding protein - human
N:Alternate names: finger protein, 275K; human immunodeficiency virus enhancer-binding
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1993 #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
C:Accession: S26661; A39829; A38253
R:Van't Veer L.J.; Lutz, P.M.; Isselbacher, K.J.; Bernards, R.
A:Title: Structure and expression of major histocompatibility complex-binding protein 2.
A:Reference number: S26661; MUID:93028387; PMID:1409593
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2500 <VANS>
X:Cross-references: EMBL:X65644; NID:938259; PIDN:CAA46596.1; PID:938260
J:BIOL. Chem. 266, 8590-8594, 1991
A:Title: HIV-EP2, a new member of the gene family encoding the human immunodeficiency vi-
A:Reference number: A39829; MUID:91217105; PMID:2022670
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 668-2144; R', 2146-2500 <NOM>
R:Rustgi, A.K.; Van't Veer L.J.; Bernards, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 8707-8710, 1990
A:Title: Two genes encode factors with NF-kappaB- and H2TF1-like DNA-binding properties.
A:Reference number: A38253; MUID:91062349; PMID:2247438
A:Molecule type: mRNA
A:Residues: 1851-1990 <KUS>
C:Genetics:
A:Cross-references: GB:M61744; GB:M33920; NID:9187404; PIDN:AAA36202.1; PID:9187405
A:Gene: GDB:HIVE2
A:Cross-references: GDB:129086; OMIM:143054
A:Map position: 6q23-6q24
C:Superfamily: HIV-EP2 enhancer-binding protein
F:242-298/Region: DNA binding; duplication; metal binding;
F:245-263/Region: DNA binding; status predicted
F:273-293/Region: zinc finger CCH motif
F:991-997/Region: zinc finger CCH motif
F:1004-1036/Region: nuclear location signal
F:1852-1908/Region: serine-rich
F:1855-1875/Region: DNA binding; status predicted
F:1883-1905/Region: zinc finger CCH motif
F:1953-1977/Region: zinc finger CCH motif

Query Match

Best Local Similarity 7.1%; Score 93.5; DB 1; Length 2500;
Matches 50; Conservative 24; Mismatches 66; Indels 47; Gaps 7;

OY 89 STDSVTEPSPVLYKNAISLPTIGSQALMLPLSPVTF-NSKQESTGPAKLPRLSCEP 147
Db 1481 STDSV-----ATLGSKMLSPASSLPLFETKQOK--RYKEEKMGQI 1523
OY 148 VMEKQOE-----KSSILENGTVHOGDTWSSGSAQSOGGRDSSLSLSPQYDWM 190
Db 1524 VEELSAVELLNDIKKDSRPQKPOLVNOGASPEKQDLOGSSSFSSLSLSPQYDWM 1583
OY 191 SLSEQPPMPAPMDND--HPPELIGKIKKESLSLDTGLSLSLQDLGLDEVLYLVNDKMK 238
Db 1584 SPSSRPPEPPPEKEMSGSRAPLPQKSGSGESKESSELDIDEMTASDMSPSSSLPA 1643
OY 239 GPSSLDE 245
Db 1644 GDGQLEE 1650

RESULT 14

T17202

DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17202
R:Van Sloun, P.P.H.; Romeijn, R.J.; Eken, J.C.J.
Mutat. Res. 433, 109-116, 1999
A:Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev3
A:Reference number: 218720; MUID:99202265; PMID:10102037
A:Accession: T17202
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3122 <VANS>
X:Cross-references: EMBL:AF083464; NID:94079830; PID:94079831; PIDN:AAC8785.1
A:Experimental source: strain 129/Ola; testis
C:Genetics:
A:Map position: 10
C:Keywords: nucleotidyltransferase

Query Match

Best Local Similarity 7.1%; Score 93.5; DB 2; Length 3122;
Matches 58; Conservative 30; Mismatches 104; Indels 45; Gaps 12;
OY 9 LKAANKRGKFKRIDLSPDM-----ISPLGDFRHHIIGKEQHDVFGDLSFLQGNV 63
Db 718 LSSGEGNKGSTLSVFPSSLTENCODLPSGGERMAH-SLESTYDESG-LNKIKIRY 775
OY 64 ELDPGNO-EKAHLGCPGCHNEFFRANSTSDSVTFETSPVLYKNAISLPTIGSQALMLPL 122
Db 776 EEFQEHKMKPSLSQAAAHYMEF-----PSVLSNCLTRP-----OK 812
OY 123 LSPVTFNSKQESFGPAKLPRLSCEPVEEKAQKESLLENGTVHOGDTWSSGSAQSOG 182
Db 813 LSPVTF-RLQSGNKPRLKLNKKKLLGLQETSTKST--ETGATKQSCCHNDLYGASKE 869
OY 183 QGRSHSSSSLS---EQLPDMAPMEDFHPPELIGKIKKESLSLDTGLSLSLQDLGLDEVLYLVNDKMK 235
Db 870 NGLSDSAKATGHTFENKRP--PLEHFD--CHGDSLSLAQSGFC-LYGNKTYLR 919

RESULT 15

T51880

Hypothetical protein DKFZP762G2015.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T51880
R:Ansorge, W.; Winkler, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, July 2000
A:Reference number: 225852
A:Accession: T51880
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-606 <AAA>
A:Cross-references: EMBL:AL390166
A:Experimental source: adult melanoma (Mewo cell line); clone DKFZP762G2015

Wed Apr 23 13:51:14 2003

us-09-806-276a-2.rpr

C:\Genetics:
A:\Note: DKFzp762c2015.1

7.0%; Score 93; DB 2; Length 606;
 Query Match 21.7%; Pred. No. 5.4; Mismatches 106; Indels 76; Gaps 11;
 Best Local Similarity 38; Conservative 61; Matches 77

```

44 IKGEGOHVVEGDIS---FLGNYELLPGNOEKA-----HLG-----Q 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 VMQGGQKGVADYDGLRVERIMSETYMLIKQVDEEALQAVKFCQVHLGLPRDRPRDPT 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 FPGHNEFFRANSTSDSVFTETPSPVLKNAISLPT-----IGSQALML--PLSPV 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 TPKHFKDSRENFPVTVVPTAPDVPADSVQRPDAHTKPRPALAAATVITTCPPSASAS 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 TFNSKQESFGPAKLPR-----LSCEPYMEKQEKSSILENGTVHOGDIS 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 TLDQSKDS-GPPRPHRPREATPSMASIGPEGKLRPEPRDGEAQAAS--ETQPLSPPTA 213
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 WGSSESASOSSQGRSH-----SSSLSEQYPD-----WPAEDMDHPTPCEL 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 ASSKAPSSGSASQPEGHPGKPEPSRAKSRPLPNMPLVTPSAATKFPPEITVTPPTTL 544
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 IKGKTSPEESLDLTGSLSLQLDLG---PSLDEVLNVMD 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 SPKGSISEETKOKLSAITSQSNANVRKESLCPALEYLE 585

```

Search completed: April 23, 2003, 11:03:23
 Job time : 20.0943 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 10:54:35 ; Search time 15.0943 Seconds
(without alignments)
697.946 Million cell updates/sec

Title: US-09-806-276a-2

Perfect score: 1326
Sequence: 1 MPAKPIYKANKNKKKKF.....QLDGLPSILDEVLYNMDKNK 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222.5	16.8	356	BOR4_HUMAN	O9H3Q1 homo sapien
2	221	16.7	349	BOR4_MOUSE	O9Jm96 mus musculu
3	195	14.7	391	MSE5_HUMAN	O00587 homo sapien
4	109.5	8.3	1475	N153_HUMAN	P49790 homo sapien
5	105	7.9	2351	FAR_HUMAN	P00451 homo sapien
6	104	7.8	1805	RWL_HUMAN	O92545 homo sapien
7	99.5	7.5	398	MAP1_SCHPO	P78926 schizosacch
8	96	7.2	825	SMI3_YEAST	P32591 saccharomyc
9	95.5	7.2	1015	FRQ_CREP	O00586 creopus spi
10	95	7.2	1833	YSR2_CAEEL	O09950 caenorhabdi
11	93.5	7.1	1322	ZEP2_HUMAN	P31629 homo sapien
12	93.5	7.1	1337	YDM5_SCHPO	O61493 mus musculu
13	92.5	7.0	1337	ITF2_HUMAN	P87136 schizosacch
14	92	6.9	667	YABD_SCHPO	P15884 homo sapien
15	90.5	6.8	899	BEM3_YEAST	O09778 schizosacch
16	90.5	6.8	1128	ACES_ELEEL	P32873 saccharomyc
17	90	6.8	633	ADYD_SCHPO	O42275 electrophor
18	89.5	6.7	510	DMN1_PARLI	O13692 schizosacch
19	89.5	6.7	1612	MYOD_XENLA	O27762 paracentrot
20	89	6.7	289	TENS_CHICK	P13904 xenopus lae
21	89	6.7	1744	ITF2_CANPA	O04205 gallus gall
22	88.5	6.7	741	CGSE_MOUSE	P15881 canis fami
23	88.5	6.7	499	YMG3_YEAST	O87080 mus musculu
24	88	6.6	478	SPG1_MOUSE	P12494 human immun
25	86	6.5	617	YMG3_YEAST	P47018 saccharomyc
26	86	6.5	1142	SGC1_HUMAN	O91182 mus musculu
27	86	6.5	1347	UTY_HUMAN	O00732 homo sapien
28	86	6.5	1189	YUH6_YEAST	O14607 homo sapien
29	85.5	6.4	1237	E75A_DROME	P17671 drosophila
30	85.5	6.4	1394	K167_HUMAN	P46013 homo sapien
31	85.5	6.4	3256	CCB2_HUMAN	O08289 homo sapien
32	85.5	6.4	660		
33	85	6.4			

34	85	6.4	2805	MAPA_HUMAN	P78559 homo sapien
35	84.5	6.4	611	IFAB_HUMAN	P23588 homo sapien
36	84.5	6.4	995	YIO9_YEAST	P04482 saccharomyc
37	84	6.3	632	CCB2_RABIT	P54288 oryctolagus
38	84	6.3	1004	SAL2_MOUSE	O9qx56 mus musculu
39	84	6.3	2148	VIT1_AEIDAE	O16927 aedes aegypt
40	84	6.3	2774	MAPA_RAT	P34926 ratius norv
41	83.5	6.3	247	TRIZ_HUMAN	P07478 homo sapien
42	83.5	6.3	356	SMR1_PODAN	O08142 podospora a
43	83.5	6.3	470	PLSB_CUCSA	O39639 cucumis sat
44	83.5	6.3	1268	PGCN_MOUSE	P35066 mus musculu
45	83	6.3	278	YD33_SCHPO	Q10267 schizosacch

ALIGNMENTS

RESULT 1
BOR4_HUMAN STANDARD; PRT; 356 AA.

AC O9H3Q1; O95828; Q96FT3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Binder of Rho GTPase 4 (Cdc42 effector protein 4).
GN BOR4 OR CEP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Ileal mucosa;
RX MEDLINE=21036164; PubMed=1185749;
RA Osada N., Kusuda J., Suzuki Y., Sugano S., Hashimoto K.;
RT "Sequence analysis, gene expression, and chromosomal assignment of
mouse Borg4 gene and its human orthologue.";
RL J. Hum. Genet. 45:374-377(2000).

RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Eye;
RX MEDLINE=21125609; PubMed=11035016;
RA Hirsch D.S., Pirone D.M., Burbelo P.D.;
RT "A new family of cdc42 effector proteins, CEPs, function in fibroblast
and epithelial cell shape changes.";
RL J. Biol. Chem. 276:875-883(2001).

RN [3]
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
RX Strausberg R.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Probably involved in the organization of the actin
cytoskeleton. May act downstream of Cdc42 to induce actin
filament assembly leading to cell shape changes. Induces
pseudopodia formation, when overexpressed in fibroblasts.

-1- SUBUNIT: Interacts with Cdc42 and Tc10, in a GTP-dependent manner
(By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated.
-1- TISSUE SPECIFICITY: Not detected in any of the adult tissues
tested. May be expressed only in fetal or embryonic tissues.

-1- SIMILARITY: BELONGS TO THE BORC/CEP FAMILY.

-1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
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CC EMBL: AB042237; BAB17272.1;
CC EMBL: AF099664; AAD16299.1;

DR EMBL: BC010451; AAH10451.1; -
 DR MIM: 603468; -
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 DR PROSITE: PS50108; CRIB; 1.
 DR Cytoskeleton.
 FT DOMAIN 27 41 CRIB.
 FT DOMAIN 70 74 POLY-SER.
 FT CONFLICT 2 2 P -> L (IN REF. 3).
 FT CONFLICT 33 33 D -> T (IN REF. 2).
 FT CONFLICT 288 288 A -> T (IN REF. 2).
 FT CONFLICT 296 296 A -> T (IN REF. 2).
 FT CONFLICT 339 339 P -> P (IN REF. 2).
 FT CONFLICT 355 355 MISSING (IN REF. 2).
 SQ SEQUENCE 356 AA; 37979 MW; 2CF677C60C6E9F1B5 CRC64;
 Query Match
 Best Local Similarity 16.8%; Score 222.5; DB 1; Length 356;
 Matches 77; Conservative 37; Mismatches 91; Indels 67; Gaps 11;
 QY 6 PLYKANKKKGKFKRLDLSPLDMSPLGFRHTIIGKGDHVGDISFLQNYEL 65
 DB 2 PLYKQVSSSVNKRKRSLADLTAEKISAPLDGFRHTMHVGRAG--DAFGDTSLNSK-- 56
 QY 66 LQNGEKAHLGQFPGHNEF-----FRANSTDSV-----FTETSPVLKN 105
 DB 57 -AGEPDGESLDEQPSSSSSKSLSRKFRGSKRSQSVTRGREGQDMGLRDSALFVK 115
 QY 106 AISTLTIGSSQALMLPLSPYTFNSKQSFPAKLPRLSCPEVMEKAKQKSSILENGT 164
 DB 116 AMSLPQLEKKA-----AEKGTSLPKSLSSPY--KKANDGSG----- 152
 QY 165 VHGGDTSSGSSASQSGRSHSS--LSEQYPPDMAPADMHDPTPCILIGKTKSEE 222
 DB 153 ---GDEAGTGEAVRRNAGAPSPPLDDEQ---AFGDLMDLPVPRATYGLKHA- 204
 QY 223 SLSDLTSLQDLGSPSLDVLNMDKNK 254
 DB 205 -----SISFHDLPSPMLGDLVLSMDKEE 229
 RESULT 2
 BORA_MOUSE
 ID BORA_MOUSE STANDARD; PRT; 349 AA.
 AC Q9JUM6; O9JUM6; 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE BLinder of Rho GTPase 4 (Cdc42 effector protein 4).
 GN BORG4 OR CEP4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=ileal mucosa;
 RX MEDLINE=21036164; PubMed=11185749;
 RA Osada N., Kusuda J., Suzuki Y., Sugano S., Hashimoto K.;
 RT "Sequence analysis, gene expression, and chromosomal assignment of
 mouse BORG4 gene and its human orthologue.";
 RL J. Hum. Genet. 45:374-377(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-143 FROM N.A., AND INTERACTION WITH TC10 AND CDC42.
 RX MEDLINE=99421943; PubMed=10490598;
 RA Joberty G., Pettinguer R.R., Macara I.G.;
 RT "The BORGs, a new family of Cdc42 and TC10 GTPase-interacting
 RT proteins.";
 RL Mol. Cell. Biol. 19:6585-6597(1999).

CC -1- FUNCTION: Probably involved in the organization of the actin
 CC cytoskeleton. May act downstream of CDC42 to induce actin
 CC filament assembly leading to cell shape changes. Induces
 CC pseudopodia formation, when overexpressed in fibroblasts.
 CC -1- SUBUNIT: Interacts with CDC42 and TC10, in a GTP-dependent manner.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: BELONGS TO THE BORG/CEP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: AB03088; BAA95932.1; -
 DR EMBL: BC003857; AAH03857.1; -
 DR EMBL: AF165114; AAD47822.1; -
 DR MGD: MGI:1929760; BORG4.
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 DR PROSITE: PS50108; CRIB; 1.
 KW Cytoskeleton.
 FT DOMAIN 27 41 CRIB.
 FT CONFLICT 143 143 K -> R (IN REF. 3).
 SQ SEQUENCE 349 AA; 37869 MW; 7C44125A7083E16B CRC64;
 Query Match
 Best Local Similarity 16.7%; Score 221; DB 1; Length 349;
 Matches 76; Conservative 42; Mismatches 83; Indels 66; Gaps 10;
 QY 6 PLYKANKKKGKFKRLDLSPLDMSPLGFRHTIIGKGDHVGDISFL-----Q 60
 DB 2 PLYKQVSSSVNKRKRSLADLTAEKISAPLDGFRHTMHVGRAG--DAFGDTSLNSKARE 59
 QY 61 GNYELLPGNOKKHLGQFPGHNEFFRANSTDSV-----FTETSPVLKNAIS 108
 DB 60 ADDESL---DEQASAKSLSLSKFRGSKRSQSVTRGREGQDMGLRDSALFVKNAIS 116
 QY 109 LPTIGSSQALMLPLSPYTFNSKQSFPAKLPRLSCPEVMEKAKQKSSILENGTVHQ 167
 DB 117 LPQLEKKA-----AEKGS--SKLPKSLSSPYKADARD----- 149
 QY 168 GDTSSGSSASQSGRSHSSLSLEQYPPDMAPADMHDPTPCILIGKTKSESDL 227
 DB 150 -----GEPKSPHNGATGPHSPPLDDEQ---AFGDLMDLPIMPKVSYGLKHA- 195
 QY 228 TGSLSLQDLGSPSLDVLNMDKNK 254
 DB 196 ---SISFHDLPSPMLGDLVLSMDKEE 220
 RESULT 3
 MSE5_HUMAN
 ID MSE5_HUMAN STANDARD; PRT; 391 AA.
 AC Q00587; Q96GNI; 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serum protein MSE55.
 GN MSE55.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92332498; PubMed=1629197;
 RA Bahou W.F., Campbell A.D., Wicha M.S.;

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CC EMBL: Z25535; CAA80982.1;
 DR Genew: HGNC:8062; NUP153.
 DR MIM: 603948;
 DR InterPro: IPR001876; Znf_RanBP.
 DR Pfam: PF00641; Znf_RanBP; 4.
 DR SMART: SM00547; Znf_RBZ; 4.
 DR PROSITE: PS01358; ZF_RANBP2_1; 4.
 DR PROSITE: PS01359; ZF_RANBP2_2; 4.
 DR Nucleic protein; Transport; Repeat; Zinc-finger; DNA-binding.
 FT DOMAIN 4 14 GLY-RICH.
 FT ZN_FING 657 687 RANBP2-TYPE 1.
 FT ZN_FING 722 751 RANBP2-TYPE 2.
 FT ZN_FING 793 822 RANBP2-TYPE 3.
 FT ZN_FING 851 880 RANBP2-TYPE 4.
 SO SEQUENCE 1475 AA; 153889 MW; 3CB415A690DF80E CRC64;

Query Match
 Best Local Similarity 26.0%; Score 109.5; DB 1; Length 1475;
 Matches 57; Conservative 31; Mismatches 86; Indels 45; Gaps 10;

QY 32 SPPLGDFPHRT-----HIGKEGQHD--VFQDISFLQNTYLLGNGEKALQCFQGN 82
 DB 953 SKPLGDFPFVGSSEKPEEYKDKNDKFKGLSSGLSNPVSLPPOFGVSNLQEEKE 1012
 QY 83 EFRANSTDS---VFETPPPV-----LKNALSLPTIGGSOALMLPLSPVFNK 131
 DB 1013 ELPRKSSAGSPFGVYINSPAPANTYIENKSSFNLTETKASAVAPFTCKTSARK 1072
 QY 132 QE-----SPG---PALPLRSCPEV--MEKAOE--KSLLENTVHQGT----- 170
 DB 1073 EEMPARKGGSPFGNEPASPSPASVFLGRTEKQEQEPVSTSLVGRKADNEPCOPV 1132
 QY 171 -SWGSSGSSASQSSQGRDSSHSSSL---SEQYDMPAEEMF 205
 DB 1133 FSGFNSQTKDENSSTKSPFSWMKPKSEOPAKATF 1171

RESULT 5
 F8_HUMAN
 ID F8_HUMAN STANDARD; PRT; 2351 AA.
 AC P00451;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor VIII precursor (Procoagulant component)
 DE (Antihemophilic factor) (AHF).
 GN F8 OR F8C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86081164; PubMed=3935400;
 RA Trueitt M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
 RA Harilog K., Kuo C.H., Maslitz F.R., Merryweather J.P., Najarian R.,
 RA Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,
 RA Urdas M.S., Valenzuela P., Dahl H.-H.M., Favalero J., Hansen J.,
 RA Nordfang O., Ezban M.;
 RT "Characterization of the polypeptide composition of human factor
 RT VIII: the nucleotide sequence and expression of the human kidney
 RT cDNA";
 RL DNA 4:333-349(1985).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86061548; PubMed=6438526;
 RA Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschler J.,
 RA Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,
 RA Delwart E., Tuddenham E.G.D., Vetter G.A., Lawn R.M.;
 RT "Expression of active human factor VIII from recombinant DNA clones";

RL Nature 312:330-337(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85061550; PubMed=6438528;
 RA Toole J.J., Knopf J.L., Mooney J.M., Sultman L.A., Buecker J.L.,
 RA Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,
 RA Amphlett G.W., Foster W.B., Coe M.L., Knutsen G.J., Fass D.N.,
 RT Hewick R.M.;
 RT "Molecular cloning of a cDNA encoding human antihemophilic factor";
 RL Nature 312:342-347(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93265012; PubMed=1303178;
 RA Gitschler J., Wood W.I.;
 RT "Sequence of the exon-containing regions of the human factor VIII
 RT gene";
 RL Hum. Mol. Genet. 1:199-200(1992).
 RN [5]
 RP SEQUENCE OF 2064-2070 FROM N.A.
 RA de Water N.S., Williams R., Browett P.J.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SUBSTITUTION OF TYR-1699.
 RX MEDLINE=91093266; PubMed=1898735;
 RA Leyte A., van Schijndel H.B., Niehrs C., Rutner W.B., Verbeet M.P.,
 RA Mertens K., van Mourik J.A.;
 RT "Substitution of Tyr1680 of human blood coagulation factor VIII is
 RT essential for the interaction of factor VIII with von Willebrand
 RT factor";
 RL J. Biol. Chem. 266:740-746(1991).
 RN [7]
 RP SUBSTITUTION.
 RX MEDLINE=92207952; PubMed=1554716;
 RA Pitman D.D., Wang J.H., Kaufman R.J.;
 RT "Identification and functional importance of tyrosine sulfate
 RT residues within recombinant factor VIII";
 RL Biochemistry 31:3315-3325(1992).
 RN [8]
 RP STRUCTURE BY NMR OF 2322-2343.
 RX MEDLINE=95200924; PubMed=7893714;
 RA Gilbert G.E., Baleja J.D.;
 RT "Membrane-binding peptide from the C2 domain of factor VIII forms an
 RT amphipathic structure as determined by NMR spectroscopy";
 RL Biochemistry 34:3022-3031(1995).
 RN [9]
 RP REVIEW ON MOLECULAR BASIS OF HEMOPHILIA A.
 RX MEDLINE=91221459; PubMed=1902642;
 RA Gitschler J.;
 RT "The molecular basis of hemophilia A";
 RL Ann. N.Y. Acad. Sci. 614:89-96(1991).
 RN [10]
 RP REVIEW ON MOLECULAR BASIS OF HEMOPHILIA A.
 RX MEDLINE=89088506; PubMed=2491949;
 RA White G.C. II, Shoemaker C.B.;
 RT "Factor VIII gene and hemophilia A";
 RL Blood 73:1-12(1989).
 RN [11]
 RP REVIEW ON MOLECULAR BASIS OF HEMOPHILIA A.
 RX MEDLINE=95245332; PubMed=7728145;
 RA Antonarakis S.E., Kazanian H.H., Tuddenham E.G.D.;
 RT "Molecular etiology of factor VIII deficiency in hemophilia A";
 RL Hum. Mutat. 5:1-22(1995).
 RN [12]
 RP VARIANT GLN-2326.
 RX MEDLINE=86235434; PubMed=3012775;
 RA Gitschler J., Wood W.I., Shuman M.A., Lawn R.M.;
 RT "Identification of a missense mutation in the factor VIII gene of a
 RT mild hemophilic";
 RL Science 232:1415-1416(1986).
 RN [13]
 RP VARIANT PRO-2135.
 RX MEDLINE=88096539; PubMed=3122181;
 RA Levinson B., Janco R.L., Phillips J.A. III, Gitschler J.;

"A novel missense mutation in the factor VIII gene identified by analysis of amplified hemophilia DNA sequences.";
 RT Nucleic Acids Res. 15:9797-9805(1987).
 RL [14]
 RN VARIANT CYN-2228; PubMed=2833855; Bell W., Griffin A.M.,
 RP MEDLINE=88191889; Antonarakis S.E.,
 RX Youssoufian H., Antonarakis S.E., Bell W., Griffin A.M.,
 RA Kazanian H.H.; missense mutations in hemophilia A: estimate of the
 RT "Nonsense and missense mutations in hemophilia A: estimate of the
 RL relative mutation rate at CG dinucleotides.";
 Am. J. Hum. Genet. 42:718-725(1988).
 [15]
 RN VARIANT GIV-291;
 RP MEDLINE=8820354; PubMed=2835904; Platakoukakis H., Kazanian H.H. Jr.,
 RX Youssoufian H., Wong C., Aronis S., Platakoukakis H., Kazanian H.H. Jr.,
 RA Antonarakis S.E.;
 RT "Moderately severe hemophilia A resulting from Glu->Gly substitution
 in exon 7 of the factor VIII gene.";
 Am. J. Hum. Genet. 42:867-871(1988).
 [16]
 RN VARIANT CYS-1708; PubMed=2499363;
 RP MEDLINE=89274393; PubMed=2499363;
 RX O'Brien D.P., Tuddenham E.G.,
 RA "Purification and characterization of factor VIII 1,689-Cys: a
 RT nonfunctional cofactor occurring in a patient with severe hemophilia
 A.";
 Blood 73:2117-2122(1989).
 [17]
 RN VARIANT CYS-391;
 RP MEDLINE=90001543; PubMed=2506948;
 RX Shima M., Ware J., Yoshio A., Fukui H., Pulcher C.A.;
 RA "An arginine to cysteine amino acid substitution at a critical
 RT thrombin cleavage site in a dysfunctional factor VIII molecule.";
 Blood 74:1612-1617(1989).
 [18]
 RN VARIANT LEU-189;
 RP MEDLINE=90057680; PubMed=2510835;
 RX Chan V., Chan T.K., Tong T.M., Todd D.;
 RA "A novel missense mutation in exon 4 of the factor VIII:C gene
 RT resulting in moderately severe hemophilia A.";
 Blood 74:2688-2691(1989).
 [19]
 RN VARIANT LEU-2326;
 RP MEDLINE=89197216; PubMed=2495245;
 RX Inaba H., Fujimaki M., Kazanian H.H. Jr., Antonarakis S.E.;
 RA "Mild hemophilia A resulting from Arg-to-Leu substitution in exon 26
 RT of the factor VIII gene.";
 Hum. Genet. 81:335-338(1989).
 [20]
 RN VARIANT HIS-391;
 RP MEDLINE=89264602; PubMed=2498882;
 RX Aral M., Inaba H., Higuchi M., Antonarakis S.E., Kazanian H.H. Jr.,
 RA Fujimaki M., Hoyer L.W.;
 RT "Direct characterization of factor VIII in plasma: detection of a
 RL mutation altering a thrombin cleavage site
 (arginine-372->histidine).";
 Proc. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).
 [21]
 RN VARIANT CYS-1708;
 RP MEDLINE=90105723; PubMed=2104766;
 RX Aral M., Higuchi M., Antonarakis S.E., Kazanian H.H. Jr.,
 RA Phillips J.A., Iii, Janco R.L., Hoyer L.W.;
 RT "Characterization of a thrombin cleavage site mutation (Arg 1689 to
 Cys) in the factor VIII gene of two unrelated patients with
 RL cross-reacting material-positive hemophilia A.";
 Blood 75:384-389(1990).
 [22]
 RN VARIANT CYN-2228 AND LEU-2326;
 RP MEDLINE=90123183; PubMed=2105106;
 RX Casula L., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,
 RA Mancuso G., Morfini M., de Biasi R., Baudo F., Cattonara A.;
 RT "Recurrent mutations and three novel rearrangements in the factor
 RL VIII gene of hemophilia A patients of Italian descent.";

Blood 75:662-670(1990).
 [23]
 RN VARIANT CYS-391;
 RP MEDLINE=90329422; PubMed=1973901;
 RX Patterson J.K., McVey J.H., Boon M., Ajani A., Tuddenham E.G.;
 RA "CRM+ haemophilia A due to a missense mutation (372->Cys) at the
 RT internal heavy chain thrombin cleavage site.";
 Br. J. Haematol. 75:73-77(1990).
 [24]
 RN VARIANT CYS-1699 AND CYS-1708;
 RP MEDLINE=90152591; PubMed=2105906;
 RX Higuchi M., Wong C., Kochan L., Olek K., Aronis S., Kasper C.K.,
 RA Kazanian H.H., Antonarakis S.E.;
 RT "Characterization of mutations in the factor VIII gene by direct
 sequencing of amplified genomic DNA.";
 Genomics 6:65-71(1990).
 [25]
 RN VARIANT CYS-1728 AND ASP-1941;
 RP MEDLINE=90169988; PubMed=2106480;
 RX Terasman M.D., Higuchi M., Kasper C.K., Antonarakis S.E.,
 RA Kazanian H.H.;
 RT "Use of denaturing gradient gel electrophoresis to detect point
 mutations in the factor VIII gene.";
 Query Match 7.9%; Score 105; DB 1; Length 2351;
 Best Local Similarity 23.0%; Pred. No. 2.1; Indels 76; Gaps 15;
 Matches 67; Conservative 46; Mismatches 102;
 5 TPYTKANNKKGKFKRLDILSPDMIS-----PVLGDFRTHIGREGODVFGDISF- 58
 818 TPNGLSLSDLEAKYETFDSDPSPGALDSNLSSEWTHRPOLH-----HS-GDMVFT 869
 59 -----LOGNYELLPGNOEKAHLGQFPGHNEFRANSTSDVTEPSPVL-----KNATS 108
 870 PRSGQLRLNKL-GTAAATELKLKLD-----FKVSTSNLSTIPSDNLAAGDNITS 922
 109 LPTIGGSOALMPLLPSPVTEKSKOES--FGPAKLPL--SCEPVWEKAKOESSILENGTV 972
 923 LG-----PSPMPHYDSQDLDTTLFGKSSPLTESGPILSSENNDSKILSGLM 222
 166 HOGDTSMGSSGASGSS-----OGRDSSSLSEOPYDPAEDMFDHPCELIKGTSEE 222
 973 NSQESSWKGKVVSTESGRLEFKRAHGPLL-----TKDNALFKVSLIKINKINSNN 1025
 223 SLSD-----LNGSLSLQDLGSPSLDEVLN-----VMDKN 253
 1026 SATNKRTHIDP--SLIENSPSYWONILSTEFKVPPLIHRMLMDKN 1074
 RESULT 6
 RML_HUMAN STANDARD; PRT; 1805 AA.
 ID C92545;
 AC 16-OCT-2001 (Rel. 4.0, Created)
 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 DT 15-JUN-2002 (Rel. 4.1, Last annotation update)
 DE RML Protein (Fragment).
 GN RML OR KIAA0257.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=bone marrow; PubMed=9039502;
 RX MEDLINE=97191544;
 RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
 RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI.
 The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
 RT analysis of cDNA clones from cell line KC-1 and brain.";
 DNA Res. 3:321-329(1996).
 CC

Query Match	Score	DB	Length
Best Local Similarity	7.8%;	104;	1805;
Matches	23.08;	1;	1805;
60; Conservative	Pred. No. 1.8;		

8 YLKAANNKGGKEFKI RDIT SDWTC... 7 mismatches 101; Indels

1062 YLEA-----OGIWEPEPRRI cun. aua. | | : | |
-----LSTFDMISPLG-----DFRHTIHICKEGCHDVFGLDIS

63 YELLPNGNOEKAHICORDDWU-----

b

1108

-----|---|---

PGHNEEFRA NSTSDSVETETPPV LKNAISLP TIGGSOAI

123 LSPVTENCWQVY
-----LSCDPCGSRGFCGAGGSSS---RPS-----AGSHKQ

```
-----GPAKLPRLSCPEVMEKAQEKSL-LENGTVHOG
: | : | : |
1140 VHDUCSUU.....
```

173 CCCCCC

```

1200 05565A5QSSQGRDSSHSSLSLSEQYPDWP-----AEDMDPDHMDPDMD
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

1200 KNSKGAKQSGHSHHSPLEQHPPRLPPVPPQBPQBPRLSPADP
317

21/ KTRSEESTDINGSLSLQLD 237

1280 ARHSSD-SDITSLTEANDKD 1279

RESULT 7

MAP1_SCHPO	.	.
L_SCHPO	.	.
STAMP_SCHPO	.	.

P78926; Q10291; 15-JUL-1998 (P01	STANDARD; PRT; 398 AA.
-------------------------------------	---------------------------

15-JUL-1998 (ver. 36, Created)
15-JUN-2003 (Rel. 36, Last sequence used)

phenomone receptor transcription factor (RefSeq: NP_001135411.1, last annotation update: 2012-07-20) (RefSeq: NP_001135411.1, last annotation update: 2012-07-20)

Factor activator (MAP1 protein).
Schizosaccharomyces pombe (Fission
Yeast) ON SPAC1E3.06.

Zakariyola; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetes.

NCBI_TaxID=4896;
Schizosaccharomycetaceae;
Schizosaccharomycetes.

11
SEQUENCE FROM N.A.

MEDLINE=966251290; PubMed=8668157;
Yabana N., Yamamoto W.

^a Schizosaccharomyces pombe map1+ encodes a gene required for cell division.

Mol. cell. Biol. 16:3420-3428(1996)

SEQUENCE FROM N.A.
MEDLINE-0715599

doi:10.1016/j.jmb.2006.05.015; PubMed=9003326; The Copenhagen School of Neuroscience

gene encodes an SBE

Genet. 253:387-392 (1996).

SEQUENCE FROM N.A.
TRAIN-972;

EDLINE=21848401; PubMed=11859360;
ood V., Gwilliam P
-1

gouros J., Peat N., Hayles J., Baker S., Pat-
brooks K., Brown D., Lyne M., Lyne R., Stewart

Bowman S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis D., Brown D., Brown S., Brown U., Basnam D.

... Davis P., Keltwell T., Fraser A.

1

[illegible][illegible]

```

Db      SOEFTSTESRAQNVFCQDNEEDNLFGEETESSVNNENANTPSIP-----INPDVN 138
OY      128 FNK-----GSEFGPAKLPRISCPEPYMEERKAOEKSSLLNGTVHOGDTISWSSSGA 178
Db      139 ENNRPAIKEDSTIQDSNGDYK---NMEDVKIOKEEP-----ENNVTIEG-----V 181
OY      179 SQSQSGRDHSISSISEOYPDPWADMDPH--TPCLLIKGTGRSESISLDTIGSLSLDL 236
Db      182 KEESO-PDENTKEMDEVIED---DEDDODPISPDSNITGDTRKSSRGLGNTTSVANTPS 237
OY      237 DLGSPLEDEVLANVDKNK 254
Db      238 ELPDAHKAEEDIETE 255

RESULT 9
PRO_CRESP ID STANDARD; PRT; 1015 AA.

AC 000586;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frequency clock protein.
FRO.
GN Cricopus spinulosus (Chromocera spinulosa).
OS Eukaryota; Fungi; Ascomycota; Petziomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OC NCBI_TaxId=110619;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FGSC 4896;
RA MEDLINE=971198515; PubMed=9037100;
RA Lewis M.T., Moran L.W., Feldman J.F.;
RT "Analysis of frequency (frq) clock gene homologs: evidence for a
RT helix-turn-helix transcription factor.";
RM 101. Funct. genet. 253:401-414(1997).
RL -1- FUNCTION: CIRCADIAN CLOCK COMPONENT INVOLVED IN THE GENERATION OF
RL BIOLOGICAL RHYTHMS. IN PARTICULAR IN RHETER STABILITY. PERIOD
RL LENGTH, AND TEMPERATURE COMPENSATION. BEHAVES AS A NEGATIVE
RL ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRO FAMILY.
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CC
DR EMBL: U25890; AAA68072.1;
KW Biological rhythms; Transcription regulation; Nuclear protein.
FT DOMAIN 240 245 POLY-SER.
FT DOMAIN 356 368 POLY-GLN.
FT FT 443 451 POLY-PRO.
FT DOMAIN 584 588 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 892 913 ASP/GLU-RICH (ACIDIC).
FT FT 1015 AA; 110972 MW; EA49EF32ED741AB1 CRC64;
SQ SEQUENCE
Query Match 7.2%; Score 95.5; DB 1; Length 1015;
Best Local Similarity 19.6%; Pred. No. 4.2; Indels 89; Gaps 10.
Matches 55; Conservative 40; Mismatches 97;

OY      26 LSPDISPLCDPFHRTHTIGKESQ-----HDVFQDISFLQGNELLPGNOE 71
Db      522 VPPDFVRANVAVDLSAKFQLSDSRDKIRMGCGDGTKFESESSEGSQSRSPENDTDENTKG 581
OY      72 KAHLGOPGHNFERRANSTDSPSVFTETPPPVKNAISPTTGGSQAQMLPLSPYTFYFK 131
Db      582 DNHKRQKTH-----STGSG-----SSGNGLPKRGQGVY-----SAS 614
OY      132 QESTFRAPKLPRISCPEPYMEERKAOEKSSLLNGTV-----HGDDTSWSSGSAOSSQ 183

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Db 615 SESFYKPL-----FLHQSPNEQSMEDGTLSPGIESNADSRWGSGSASNR 667
QY 184 GR-----DSHSSSLSPQYDPMPAEPMFHPHPPCLING 216
Db 668 KRRRDGALIIYSGAPFCTDLSGPGTSPATYMLSSERERD--AQQGFARPLFRSSGG 725
QY 217 KTKSEESLSP-----TSSLSLQ-LDGLPSLDEVLYNVDKN 253
Db 726 SSIRRLSPDAHLNLSIPIKQLLNEGVSIPELVTDGDS 766

RESULT 10
YSR2 CAEEL
ID YSR2 CAEEL STANDARD; PRT; 482 AA.
AC 009550;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hypothetical 54.6 kDa protein F59B10.2 in chromosome II.
GN F59B10.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OX Rhabditidae; Pelodierinae; Caenorhabditis.
RN NCBI_TaxID:6239;
RP SEQUENCE FROM N.A.
RA STRAIN-Bristol N2;
RU Lloyd C.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@isb-sib.ch).
DR EMBL; Z48716; CAAB8601.1;
DR Wormpep; F59B10.2; CE01591.
KW Hypothetical protein.
FT DOMAIN 214 282
FT DOMAIN 228 241 SER-RICH.
FT DOMAIN 276 282 POLY-SER.
FT DOMAIN 378 384 POLY-SER.
FT DOMAIN 397 412 POLY-SER.
FT DOMAIN 404 412 ARG-RICH.
SQ SEQUENCE 482 AA; 54641 MW; 1BD7DJ3E9DDAA74B CRC64;

Query Match
Best Local Similarity 23.6%; Score 95; DB 1; Length 482;
Matches 65; Conservative 33; Mismatches 99; Indels 78; Gaps 12;

QY 1 MPATPIYLAANKKKKFF-----KLDDILSPMISPLGDRRHITHGKES-QHDVYG 54
Db 68 LPLGTF-----GQVGRSLMDIRELNISDOLIKPELKKMLRKAKGESKRHAHE 121
QY 55 DISFLDGNTELLPGNOEKAHGQFGNHEPFA-----NSTSDS-----VETL-PSPV 102
Db 122 SIOEEKISIEDLP-----TAQLPSKSPKKAIGSGSSSDSLIDDEVFEVLSPP 174
QY 103 LKNALSLPTIGSSQALMLPLSPITFNSKQESFGPAKLRCLSCPEVMEKQOE-----156
Db 175 RKPADA-----RTAPVVEKKIEK-PA-----VKEQAKKKKKETPT 210
QY 157 -----SLLNGCVHOGDTSMGSSGASOSQGDHSSLSLQYDPMPAEPMFHPHPP 210
Db 211 PTESEFSSSSSSSTSSSTSSSSSSSASSESESEKSSQVSSSKTSTSKAASSKAYGSD 270
QY 211 CELIKGKTKGKEESLDTGLSLSLQDLQPSLDE 245
Db 271 FESEKSSSSSASTISKVT-----PKKDK 294

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RESULT 11
ID ZEP2_HUMAN STANDARD; PRT; 1833 AA.
AC P31629;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-JUL-1993 (Rel. 26, Last sequence update)
DE Human Immunodeficiency virus type 1 enhancer-binding protein 2
DE (HIV-Ep2).
GN HIVEB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID:9606;
RP SEQUENCE FROM N.A.
RA MEDLINE-91217105; PubMed-2022670;
RA Nomura N., Zhao M.-J., Nagase T., Maekawa T., Ishizaki R., Tabata S.,
RA Ishii S.;
RT "HIV-Ep2, a new member of the gene family encoding the human
RT immunodeficiency virus type 1 enhancer-binding protein. Comparison
RT with HIV-Ep1/PRDII-BP1/MBP-1."
RL J. Biol. Chem. 266:8590-8594(1991).
RN (2)
RP SEQUENCE OF 1184-1323 FROM N.A.
RA MEDLINE-91062349; PubMed-2247438;
RA Rustgi A.K., Van T. Veer L.J., Bernards R.;
RT "Two genes encode factors with NF-kappa B- and H2TF1-like DNA-binding
RT properties."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8707-8710(1990).
CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC 5'-GGGACCTTC-3', WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV.
CC OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC IN T-CELL ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC -1- SIMILARITY: STRONG, TO HIVEB1.
CC -----
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CC or send an email to license@isb-sib.ch).
DR EMBL; M60119; AAB88218.1;
DR EMBL; M61744; AAA36202.1;
DR PIR; A39829; WMH0E2.
DR HSSP; P15822; 1BBO.
DR TRASPAC; T00939;
DR Genew; HGNC:4921; HIVEB2.
DR MIM; 143054;
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00026; ZINC_FINGER_C2H2_1; 2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
KW Nuclear protein; Repeat.
FT DOMAIN 324 330 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 337 369 SER-RICH.
FT DOMAIN 1286 1310 ASP/GLU-RICH (ACIDIC).
FT ZN-FING 1186 1208 C2H2-TYPE.
FT ZN-FING 1214 1238 C2H2-TYPE.
SQ SEQUENCE 1833 AA; 202128 MW; BAF0FA37B075C23 CRC64;

Query Match
Best Local Similarity 26.7%; Score 93.5; DB 1; Length 1833;
Matches 13;

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Matches 50: Conservative 24: Mismatches 66: Indels 47: Gaps 7:

QY 89 STSDSVETTPSPVKNALSLPTIGSQALMLPLSPVTF-NSKQESGPAKRLRSCPE 147
 DB 814 STDSV-----ATLGGSKRMISPASSLFETKQOK--RKKEKMGQOI 856
 QY 148 VMEKAO-----KSLLENGTVHQ---GDTSMGSGASQSQGRDSSHS 190
 DB 857 VEELSAVELNSDIKRLSPKPOLYRQGCASEPKDQSGSSSSSLSPSSQDYPVS 916
 QY 191 SLSEQYDPAEDMFD---HPPELILKTKTKSESS-----LSDTGSLSLQIDL 238
 DB 917 SPSSSEPPPEKMLSGRAFLPQKSSGSSKSSSDELDIDETASDMSPQSSSLPA 976
 QY 239 GPSLDE 245
 DB 977 GGQLE 983

RESULT 12
 PROZ_MOUSE
 ID DPOZ_MOUSE STANDARD: PRT: 3122 AA.
 AC 061493; 09QW6; 09JMD6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related protein 4).
 GN REV3L OR POLZ OR SEZ4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola; TISSUE=Testis;
 RX MEDLINE=99202265; PubMed=10102037;
 RA Van Sloun P.P.H., Romelijn R.J., Bekken J.C.J.;
 RT "Molecular cloning, expression and chromosomal localisation of the mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
 RT Mutat. Res. 433:109-116(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Kajiwara K.;
 RT "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in brain neurons.";
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE OF 2368-3122 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic brain;
 RX MEDLINE=96216731; PubMed=8645260;
 RA Kajiwara K., Nagawara H., Shimizu-Nishikawa K., Ookura T., Kimura M., Sugaya E.;
 RT "Molecular characterization of seizure-related genes isolated by differential screening.";
 RT Biochem. Biophys. Res. Commun. 219:795-799(1996).
 RL [4]
 RN BIOCHEM. ACTIVITY: N deoxynucleoside triphosphate - N diphosphate + (DNA)(N)
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
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 CC EMBL: AF083464; AAC98785.1;
 CC EMBL: AB031049; BAA90768.1;
 CC EMBL: D78644; BAA11461.1;
 CC MGI: MGI:1337131; Rev31.

DR InterPro: IPR002064; DNA_POL_B.
 DR InterPro: IPR004578; Pol2.
 DR Pfam: PF00136; DNA_POL_B; 2.
 DR Pfam: PF03104; DNA_POL_B-exo; 2.
 DR PRINTS: PR00106; DNAPOLB.
 DR SMART: SM00486; POLBc; 1.
 DR TIGRfam: TIGR00592; Pol2; 1.
 DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
 DR Transferrase; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; DNA repair; Nuclear protein; zinc-finger.
 FT ZN-FING 3034 3049
 FT ZN-FING 3078 3096
 FT CONFLICT 92 92 G->A (IN REF. 2).
 FT CONFLICT 294 294 A->T (IN REF. 2).
 FT CONFLICT 578 578 E->Q (IN REF. 2).
 FT CONFLICT 609 609 R->Q (IN REF. 2).
 FT CONFLICT 1278 1278 L->P (IN REF. 2).
 FT CONFLICT 1298 1298 L->F (IN REF. 2).
 FT CONFLICT 1416 1416 P->T (IN REF. 2).
 FT CONFLICT 1848 1848 A->T (IN REF. 2).
 FT CONFLICT 2368 2368 V->G (IN REF. 3).
 SQ SEQUENCE 3122 AA; 350654 MW; A39846CAF73655A8 CRC64;

Query Match 7.1%; Score 93.5; DB 1; Length 3122;
 Best Local Similarity 24.5%; Pred. No. 27;
 Matches 58: Conservative 30; Mismatches 104; Indels 45; Gaps 12;

QY 9 IKAANNKKKKFKRLDILSPDM-----ISPLGDFRHTTHIGEGOHVFGDISFLQGNV 63
 DB 718 LSEGENEKNGSTSLSGVPSSTLNCDLPSGSENSMAH-SLESTIDBSG-LINKTKIRY 775
 QY 64 ELLPNO-EKAHLGEPGNEFFRANSTSDVETTPSPVKNALSLPTIGSQALMLPL 122
 DB 776 EEPQEHKMEKPSLSQAAHYMF-----PSVLISLCVLRP-----QK 812
 QY 123 LSPVTNSKQESFGPAKRLRSCPEYMEKQKESLLENGTVHQDPTSWGSSGASQSS 182
 DB 813 LSPVTV-KLQSNKPSRLKLNKKLIGLEISTST--ETGATDCSTQHDLYTGASEKE 869
 QY 183 QGRDSSSSSS-----EYQPDPAEDMFDHPPELILKTKTKSESSLSLQIDL 235
 DB 870 NGLSDSAKRTHOTFENKP--PTEHRID---CHRGDSLAEQSFQ-LIGNKTYTLR 919

RESULT 13
 YDM5_SCHPO
 ID YDM5_SCHPO STANDARD: PRT: 1337 AA.
 AC P87136;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C57A7.05 in chromosome I.
 GN SPC57A7.05.
 OS Schizosaccharomyces pombe (fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sounos J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Mouton L., Mungall K., Murphy L., Niblett D., Odeli C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vansteels E., Rieger M., Schaefer M., Meller-Auer S.,
 RA Gabel C., Fuchs I., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambach R., Punelle B.,
 RA Goffeau F., Aves S.J., Dreano S., Gloux S., Lelaune V., Motter S.,
 RA Lucas M., Koehet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RA "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: SOME, TO YEAST YDL231C.
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 CC -----
 DR EMBL: 295396; CAB08763.1; -
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 209 229
 FT TRANSMEM 241 261 POTENTIAL.
 FT TRANSMEM 267 287 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 387 407 POTENTIAL.
 FT TRANSMEM 917 937 POTENTIAL.
 FT TRANSMEM 975 995 POTENTIAL.
 FT TRANSMEM 997 1017 POTENTIAL.
 FT TRANSMEM 1021 1041 POTENTIAL.
 FT TRANSMEM 1066 1086 POTENTIAL.
 FT TRANSMEM 1275 1295 POTENTIAL.
 SQ SEQUENCE 1337 AA; 150848 MW; A549BC8ED0D08791 CRC64;
 Query Match Best local similarity 7.0%; Score 92.5; DB 1; Length 1337;
 Matches 48; Conservative 20; Mismatches 68; Indels 33; Gaps 9;
 QY 67 PENQEKALGQPPGHNFFRANSTDSVFTTSPVYK--NAISLPTI---GGSQALM 119
 DB 7 PNLDRAN-AQL--SNISTESSSSNSTRASGSRHVKATSNRVSLLPIKIGKSPPAIR 63
 QY 120 LPLSPVTFENKQ-----ESFGPAKLPLRSCFVMEKQKES-----SLANGIV----- 165
 DB 64 QPTESSTHFQSSHSVNAHNOQSPINQSSGSSANVFTFEINDEPSPFNNSFFKNDARDIP 123
 QY 166 ----HGDITWSSGSSGSSGSSGSSGSSSLSDQYDPAEDMFDHP 210
 DB 124 QQPSHSQNPSSSSSSSSSSSSQSSQ-----HSHLQRPQIPSNKSKL--DDPSP 167
 RESULT 14
 ID ITF2_HUMAN STANDARD: PRT; 667 AA.
 AC P15884; Q15439; Q15440;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-APR-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Transcription factor 4 (Immunoglobulin transcription factor 2) (ITF-2)
 DE Transcription factor 4 (Immunoglobulin transcription factor 2) (ITF-2)
 GN TCF4 OR ITF2 OR SEF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SEF2-1A AND SEF2-1B).
 RC TISSUE=thymocytes;
 RA MEDLINE=92013505; PubMed=1681116;
 RA Corneliussen B., Thornell A., Hallberg B., Grundstrom T.,
 RT "Helix-loop-helix transcriptional activators bind to a sequence in
 RT glucocorticoid response elements of retrovirus enhancers."
 RL J. Virol. 65:6084-6093(1991).
 RN [2]
 RP SEQUENCE OF 46-667 FROM N.A. (ISOFORM SEF2-1B).
 RX MEDLINE=90175016; PubMed=2308860;
 RA Henthorn P., McCarrick-Walmsley R., Kadesch T.,
 RT "Sequence of the cDNA encoding ITF-2, a positive-acting transcription
 RT factor."
 RL Nucleic Acids Res. 18:678-678(1990).
 RN [3]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=90140708; PubMed=2105528;
 RA Henthorn P., Kiledjian M., Kadesch T.,
 RT "Two distinct transcription factors that bind the immunoglobulin
 RT enhancer micro5/kappa 2 motif."
 RL Science 247:467-470(1990).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IMMUNOGLOBULIN
 CC SOMATOSTATIN RECEPTOR 2 INITIATOR ELEMENT (SSTR2-IR) TO ACTIVATE
 CC TRANSCRIPTION (BY SIMILARITY). PREFERENTIALLY BINDS TO EITHER 5'-
 CC ACANNTGT-3' OR 5'-CCANNTGC-3'.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. FORMS HOMO- OR HETERO-OLIGOMERS WITH MYOGENIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; SEF2-1A, SEF2-1B (SHOWN
 CC HERE) AND SEF2-1D; ARE PRODUCED BY ALTERNATIVE SPLICING. IN
 CC ADDITION, A MINI-EXON CODING FOR FOUR AMINO ACIDS MAY OR MAY NOT
 CC BE INCLUDED.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT HEART, BRAIN, PLACENTA,
 CC SKELETAL MUSCLE AND TO A LESSER EXTENT IN THE LUNG. IN DEVELOPING
 CC EMBRYONIC TISSUES, EXPRESSION MOSTLY OCCURS IN THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
 CC -----
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 CC -----
 DR EMBL: M74718; AA60310.1; -
 DR EMBL: M74719; AA60311.1; -
 DR EMBL: X52079; CA6298.1; -
 DR PIR: S08461; S08461.
 DR TRANSFAC: T00433; -
 DR GeneW: HGNC:11634; TCF4.
 DR MIM: 602272; -
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH_1.
 DR SMART: SM00353; HLH_1.
 DR PROSITE: PS00036; HLH_1; 1.
 DR PROSITE: PS50888; HLH_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Alternative splicing.
 FT DOMAIN 1 83
 FT DOMAIN 228 231
 FT DOMAIN 379 400
 FT DNA_BIND 564 576
 FT DOMAIN 577 618
 FT DOMAIN 642 642
 FT VARSPIC 177 183
 FT VARSPIC 545 545
 FT CONFLICT 46 49
 FT CONFLICT 334 334
 P -> S (IN REF. 2).
 ESSENTIAL FOR MYOD INHIBITION (BY
 SIMILARITY).
 POLY-SER.
 LEUCINE-ZIPPER (POTENTIAL).
 BASIC DOMAIN.
 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CLASS A SPECIFIC DOMAIN.
 PRGIPSS -> RYNGKA (IN ISOFORM SEF2-1A).
 T -> TRSR (IN ISOFORM SEF2-1D).
 TGSN -> EFGG (IN REF. 2).
 P -> S (IN REF. 2).

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CC EMBL; 254285; CAA91078.1;
CC HYPOTHETICAL protein; Transmembrane
DK 70 POTENTIAL
FT 358 POTENTIAL
FT TRANSMEM 338 358
FT TRANSSEM 103435 MW; 03D/E9CC8866ECAB CRC64;
SEQUENCE 899 AA; 6.8%; Score 90.5; DB 1; Length 899;
SQ
Query Match Similarity 24.7%; 26; Mismatches 33; Gaps 8
Best Local 48; Conservative 6.8%; Pred. No. 9.2; 85; Indels 33; Gaps 8
Matches 48; Conservative 6.8%; Pred. No. 9.2; 85; Indels 33; Gaps 8
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QY 62 NYELLPCNDKEKHLGCFPHGNHFRANS-----TSDSVTEFTPS-PYKNAISLPTGSGQ 116
DB 377 NOELL-STKDGGLGHHLAHNSFLKTYTAELETLPKSRMLDLSIAVVALCNSLNVGLAE 435
QY 117 ALMLPL--LSYFENSKOESFGPAKLR-----LSCPEYMEKROEKSLLNGTYHQGT 492
DB 436 SVMDPFGKLPFTTETTSATGLIAYVNESHDIASEPSSIMPNPSI--SSSVASATV 224
QY 171 SWSSSGSASQSSQGDHSSLSSEQYDWPDAEDMPPHPTPCILGKTKS-----EESL 224
DB 493 FDKAKLNTEDSYDNTSHGTSISEV-----SSHVHYGERSNNLELTSESL 540
QY 225 SDLTGLSLTQLDL 238
DB 541 SSTNDTIRLRQRL 554

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Search completed: April 23, 2003, 11:01:43
Job time : 19.0943 secs

	RESULT 15		PRT:	899 AA.
YABD_SCHPO	STANDARD:			
ID	YABD_SCHPO			
AC	009778;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 41, Last annotation update)			
DT	15-JUN-2002 (Rel. 41, Last chromosome I.)			
DT	Hypothetical protein C22F3.13 in chromosome I.			
DE	SPAC22F3.13			
GN	Schizosaccharomyces pombe (fission yeast).			
OS	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetales; Schizosaccharomycetes.			
OC	Schizosaccharomycetes.			
CC	NCBI_TaxID=4896;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RC	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gilliam R., Hayles J., Basham D., Bowman S.,			
RA	Medwin P., Peat N., Chillingworth T., Churcher C.N.,			
RA	Brown D., Brown M., Davis P., Haldon J., Hodgson G.,			
RA	Brooke K., Connor R., Cronin A., DAVIS P., Hidalgo J., Jagels K.,			
RA	Collins S., Goble A., Hamlin N., Harris D.J., Hunt S., Jagers K.,			
RA	Gentile S., Hornsby T., Howarth S., Huckle E., McLean U.,			
RA	Holtorf S., Jones L., Jones M., Leather S., McDonald S., Odeil C.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., Odeil C.,			
RA	Mooney K., Moule S., Munagall K., Murphy L., Niblett D., Odeil C.,			
RA	Olyver K., O'Neill S., Pearson D., Quail M.A., Rablowski E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger S., Stevens K.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Warren T., Whitehead S.,			
RA	Taylor K., Taylor R.G., Tyler A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodsward J., Volkarski E., Aert R., Robben J., Grymposre B., Hilbert H.,			
RA	Wellens I., Vanstreels E., Hogler E., Moestl D.T.R., Pohl T.M.,			
RA	Gabel C., Fuchs M., Fritz C., Lechner H., Reinhardt B.,			
RA	Borzym K., Lager I., Beck A., Mamut R., Purrelle B.,			
RA	Eger P., Zimmermann W., Wedler H., Gloux S., Lelaire V., Motter S.,			
RA	Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,			
RA	Gallbert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Daga R.R., Cruzuelo L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,			
RA	Cerritelli L., Lowe T., McCombie M.K., Paulsen I., Potashkin J.,			
RA	Domiguez A., Kuyvela J.L., Moreno S., Armstrong J., Potashkin J.,			
RA	Shpakovski G.V., Usery D., Barrett B.G., Nurse P.;			
RI	"The genome sequence of Schizosaccharomyces pombe".			
RL	Nature 415:871-880(2002). Integral membrane protein (Potential).			
CC	-1 SUBCELLULAR LOCATION:			
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111

Query Match
Best Local Similarity 100.0%; Score 1326; DB 4; Length 254;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
DB 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
OY 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
DB 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
OY 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
DB 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
OY 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
DB 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
OY 241 SLIDEVLAVMDKNK 254
DB 241 SLIDEVLAVMDKNK 254

RESULT 2

ID 095353 PRELIMINARY; PRT; 254 AA.
AC 095353;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DE 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DE MSE5-related protein.
GN UBL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE=98204843; PubMed=9535835;
RT "Analysis of Rhox-binding proteins reveals an interaction domain
RT conserved in heterotrimeric G protein beta subunits and the yeast
RL J. Biol. Chem. 273:8616-8622(1998).
DR EMBL: AF094521; AAC71773.1; -
DR InterPro: IPR000095; PAKbox/Rhobindng.
DR SMART: SM00285; PBD: 1.
SQ SEQUENCE 254 AA; 27738 MW; C31CDBEL5IDA605D CRC64;

Query Match

Best Local Similarity 99.5%; Score 1320; DB 4; Length 254;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
DB 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
OY 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
DB 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
OY 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
DB 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
OY 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
DB 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
OY 241 SLIDEVLAVMDKNK 254

DB 241 SLIDEVLAVMDKNK 254

RESULT 3

ID 090010 PRELIMINARY; PRT; 254 AA.
AC 090010;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE Cdc42 effector protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PREGNANT UTERUS;
RA MEDLINE=21125609; PubMed=11035016;
RT "A New Family of Cdc42 Effector Proteins, CEPs, Function in Fibroblast
RT and Epithelial Cell Shape Changes."
RL J. Biol. Chem. 276:875-883(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PREGNANT UTERUS;
RA Thomas D.S.; Burdello P.D.;
RT "Unique domains define a new family of Cdc42 effector proteins
RT (CEPs)."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF104857; AAD16888.1; -
DR InterPro: IPR000095; PAKbox/Rhobindng.
DR SMART: SM00285; PBD: 1.
SQ SEQUENCE 254 AA; 27679 MW; DBC2886CDAC7B822 CRC64;

Query Match

Best Local Similarity 99.5%; Score 1319; DB 4; Length 254;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
DB 1 MPATPTIYKAANNKGGKFKRLDILSPDMISPLDGFRTTHIGKEGHDVFGDISLQ 60
OY 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
DB 61 GNYELLPGNOEKALHGOFPGHNEFFRANSTSDSVFETETSPVLAIAISLPTIGSSQALML 120
OY 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
DB 121 PLISPTVFNKQESFGPAKLPRLSCPEVMEKAKQESSLLENGTVHOGDTSMGSSGSAQ 180
OY 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
DB 181 SSQGRSHSSLSSEQYPDMPADMDHPTPELILKGTKEESLSLQSLSLQDLIGP 240
OY 241 SLIDEVLAVMDKNK 254
DB 241 SLIDEVLAVMDKNK 254

RESULT 4

ID 090005 PRELIMINARY; PRT; 254 AA.
AC 090005;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE 3200001F04RIK protein (RIKEN cDNA 3200001F04 gene).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD, AND EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawaji T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaitanari M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK019447; BAB31723.1; -;
 DR EMBL: AK012309; BAB28155.1; -;
 DR EMBL: AK014281; BAB29241.1; -;
 DR EMBL: BC021409; AAB21409.1; -;
 DR MGI:1915275; 3200001F04Rik;
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 SO SEQUENCE 254 AA; 27686 MW; 9EB9991CF1EB678F CRC64;
 Query Match 92.8%; Score 1230; DB 11; Length 254;
 Best Local Similarity 92.5%; Pred. No. 2,7e-106;
 Matches 235; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 OY 1 MPAPPIYLKANKKKGKFKRLDILSPDMISPLDGFRTTHIGKEGQHDVFGDISFLQ 60
 DB 1 MPAPPIYLKANKKKGKFKRLDILSPDMISPLDGFRTTHIGKEGQHDVFGDISFLQ 60
 OY 61 GNYELLPGNOKA--HGQPGHNEFFRANSTSDSVTFETPPSPVLNNAISLPTIGSQAL 120
 DB 61 GNYELLPGNOKA--HGQPGHNEFFRANSTSDSVTFETPPSPVLNNAISLPTIGSQAL 120
 OY 121 PLTSPVTFNSKQESFGPAKLPRLSCPEPYMEKAEKSSILENGTVHOGDTSMGSSGSASQ 180
 DB 121 PLTSPVTFNSKQESFGPAKLPRLSCPEPYMEKAEKSSILENGTVHOGDTSMGSSGSASQ 180
 OY 181 SSGGRDSSSSLSLSEQYPDWPAEDMFDPCELIKTKTSSESISLDTGSLISLQDLGP 240
 DB 181 SSGGRDSSSSLSLSEQYPDWPAEDMFDPCELIKTKTSSESISLDTGSLISLQDLGP 240
 OY 241 SLIDEVLANMDKN 254
 DB 241 SLIDEVLANMDKN 254
 RESULT 5
 O14613 PRELIMINARY; PRT; 210 AA.
 AC 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 22.5 kDa protein (Cdc42 effector protein 2).
 GN BORG1.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97397562; PubMed=9253601;
 RX Gurr S.C., Agarwal S.K., Manickam P., Olufemi S.-E., Crabtree J.S.,
 RA Weisemann J.M., Kester M., Kim Y.S., Emmert-Buck M.R., Liotta L.A.,
 RA Spiegel A.M., Bouski M., Roe B.A., Collins F.S., Burns A.L.,
 RA Marx S.J., Chandrasekharappa S.C.;
 RT "A transcript map for the 2.8-Mb region containing the multiple
 RT endocrine neoplasia type 1 locus.";
 RT Genome Res. 7:725-735(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=WHOLE BRAIN;
 RX MEDLINE=99421943; PubMed=10490598;
 RA Joderty G., Peilungher R.R., Macara I.G.;
 RT "The Borgs, a new family of Cdc42 and Rac1 GTPase-interacting
 RT proteins.";
 RT Mol. Cell. Biol. 19:6585-6597(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF001436; AAB81206.1; -;
 DR EMBL: AF163840; AAD48784.1; -;
 DR EMBL: BC022337; AAB22337.1; -;
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 KW Hypothetical protein.
 SO SEQUENCE 210 AA; 22483 MW; 7755100672FFB69C CRC64;
 Query Match 30.7%; Score 407.5; DB 4; Length 210;
 Best Local Similarity 41.2%; Pred. No. 6,6e-30;
 Matches 107; Conservative 23; Mismatches 65; Indels 65; Gaps 8;
 OY 1 MPAPPIYLKANKKKGKFKRLDILSPDMISPLDGFRTTHIGKEGQHDVFGDISFLQ 60
 DB 1 MSTKVPPIYLK-RGSRKKEKRLDILSSDMISPLDGFRTTHIGSGGSDMGDISFLQ 59
 OY 61 GNYELLPGNOKA--HGQPGHNEFFRANSTSDSVTFETPPSPVLNNAISLPTIGSQAL 118
 DB 61 GNYELLPGNOKA--HGQPGHNEFFRANSTSDSVTFETPPSPVLNNAISLPTIGSQAL 118
 OY 119 MLPLSPVTFNSKQESFGPAKLPRLSCPEPYMEKAEKSS-----LLENGTVHOGDTSMG 173
 DB 120 TLPTAQ-----APKPPRLHL-TPQSPQGGGSDIWRIPETGSPNSGTL--- 164
 OY 174 SSGSASQSGGRDSSSSLSLSEQYPDWPAEDMFDPCELIKTKTSSESISLDTGSLIS 233
 DB 165 -----PESGAEPF-----LSN-ASSLIS 182
 OY 234 LQDLGSPSLDEVLANMDKN 253
 DB 183 LHYDLGSPSLDEVLANMDQ 202
 RESULT 6
 O9UNSO PRELIMINARY; PRT; 210 AA.
 AC 09UNSO;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cdc42 effector protein 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
 RA MEDLINE=99362714; PubMed=10430899; Spiegel S.;
 RT Boubero P.D., Snow D.M., Bahou W., "MESE5, a Cdc42 effector protein, induces long cellular extensions in
 RT fibroblasts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:9083-9088(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=21125609; PubMed=11035016;
 RA Hirsch D.S., Pitone D.M., Burbello P.D.,
 RT "A New Family of Cdc42 Effector Proteins, CEPs, Function in Fibroblast
 RT and Epithelial Cell Shape Changes.";
 RL J. Biol. Chem. 276:875-883(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Thomas D.S., Burbello P.D.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF098290; ADD16185.1; -;
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 SQ SEQUENCE 210 AA; 22479 MW; 8255100667FEB936 CRC64;

Query Match 30.7%; Score 406.5; DB 4; Length 210;
 Best Local Similarity 41.2%; Pred. No. 8.2e-30;
 Matches 107; Conservative 23; Mismatches 65; Indels 65; Gaps 8;

OY 1 MPAKTPYLKAAANKKFKLRLDILSPDMSPLGLDFRHTTHIGEGQHVFGDISLQ 60
 DB 1 MSTKVPYLYL-RGSRKCKEKLRLDILSPDMSPLGLDFRHTTHIGEGQHVFGDISLQ 59
 OY 61 GNYELLPGNQEKA--HIGQFPGHNEFFRANSTSDVFTETPSVLKNAISLPTTIGSQAL 118
 DB 60 GKPHLLPGTGWEGPEEGEDFEDLPFGFTATATVCGRELPGSPPLKNAISLPIVIGPQAL 119
 OY 119 MLPPLSPVTNSQESFGPAKLRLSCPEVMEKQEKSS-----LLNGVHVGQDTSWG 173
 DB 120 TLPTAQ-----APPKPRHLHE-TPOPSPQEGGSVDIMRIPTGSPNSGLT--- 164
 OY 174 SSGSASQSSQGRDSSSLSEQYPPWPAEDMFDHPTECLIKGKTKSEESLSDLTGSILS 233
 DB 165 -----PESGAEEPF-----LSN-ASSILS 182
 OY 234 LQDLGSPILDEVLTVMQDN 253
 DB 183 LHVLDGSPILDEVLTVMQDN 202

RESULT 7

OY9BS13 PRELIMINARY; PRT; 210 AA.
 AC OY9BS13;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2002 (TREMblrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Cdc42 effector protein 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CERVIX;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005406; AA05406.1; -;
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR SMART: SM00285; PBD; 1.
 SQ SEQUENCE 210 AA; 22456 MW; 775500887C0FB69C CRC64;

Query Match 30.7%; Score 406.5; DB 4; Length 210;
 Best Local Similarity 41.2%; Pred. No. 8.2e-30;

Matches 107; Conservative 22; Mismatches 66; Indels 65; Gaps 8;
 OY 1 MPAKTPYLKAAANKKFKLRLDILSPDMSPLGLDFRHTTHIGEGQHVFGDISLQ 60
 DB 1 MSTKVPYLYL-RGSRKCKEKLRLDILSPDMSPLGLDFRHTTHIGEGQHVFGDISLQ 59
 OY 61 GNYELLPGNQEKA--HIGQFPGHNEFFRANSTSDVFTETPSVLKNAISLPTTIGSQAL 118
 DB 60 GKPHLLPGTGWEGPEEGEDFEDLPFGFTATATVCGRELPGSPPLKNAISLPIVIGPQAL 119
 OY 119 MLPPLSPVTNSQESFGPAKLRLSCPEVMEKQEKSS-----LLNGVHVGQDTSWG 173
 DB 120 TLPTAQ-----APPKPRHLHE-TPOPSPQEGGSVDIMRIPTGSPNSGLT--- 164
 OY 174 SSGSASQSSQGRDSSSLSEQYPPWPAEDMFDHPTECLIKGKTKSEESLSDLTGSILS 233
 DB 165 -----PESGAEEPF-----LSN-ASSILS 182
 OY 234 LQDLGSPILDEVLTVMQDN 253
 DB 183 LHVLDGSPILDEVLTVMQDN 202

RESULT 8

OY9DBM1 PRELIMINARY; PRT; 409 AA.
 AC OY9DBM1;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2002 (TREMblrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE 1810058K22RIK protein.
 GN 1810058K22RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE-PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombearts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK007896; BAB25335.1; -;
 DR MGI: 1917061; 1810058K22RIK.
 DR InterPro: IPR000095; PAKbox/Rhobndng.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR SMART: SM00285; PBD; 1.
 SQ SEQUENCE 409 AA; 43064 MW; 7444DB005B1AEB1 CRC64;

Query Match 16.3%; Score 216; DB 11; Length 409;
 Best Local Similarity 32.5%; Pred. No. 1.1e-11;
 Matches 82; Conservative 26; Mismatches 62; Indels 82; Gaps 14;
 OY 26 LSPDMISPLGDRHTTHIGEGQHVFGDISL-----GNYELLPGN-----QEKA 73

[illegible]

DR PROSITE: P550011; PROTEIN KINASE DOM; 1.
 DR PROSITE: P500109; PROTEIN KINASE TYR; UNKNOWN; 1.
 DR PROSITE: P500589; PTS_LHR_SER; UNKNOWN; 1.
 KW ATP-binding; P500501; SPASE_1; UNKNOWN; 1.
 SO SEQUENCE 1337 AA; 147476 MW; 126509DF5A82724 CMC64;

Query Match
 Best Local Similarity 9.8%; Score 130.5; DB 5; Length 1337;
 Matches 63; Conservative 34; Mismatches 103; Indels 59; Gaps 13;

QY 1 MPKPTIYLKANKKGRKFKRLDILSPDILGDFHRTHTIKESQHDVEGDISL-59
 DB 462 LPSSTDFSEFVSQHSRISKRLR-----TMSKPNQNDPKHGVHIDGA--TEGDIATLG 515
 QY 60 -QGVNELLPGNKEAHGQPGHNEFRANSTDSVFTEP---SPVLKNAISLPFGGS 115
 DB 516 SSGYNNV-----KQIYVYKPSEDI-EQTPILLPTPTSPSLQTAGS- 559
 QY 116 QALMLPLSPVFN-----KQSFPAKLPRLSCPEVMEKAEKSSLENGTV-----HQ 167
 DB 560 -----TPPGANGSGAMGTSMNPTPTPSAEHTPLATVNGQSFPAQSTNPPPNK 612
 QY 168 GPTWSSGSSASQSGRSHSSLSLEQYPPADMDHPTPELTKIKKEESLSD- 227
 DB 613 GDDLE-FEGGHNYGADGKVSSET-----GM-----RPTSRIVDPHEHRTSD- 657
 QY 228 TGSLLSLDLDLPSILDEV 246
 DB 658 --EIAADKIDFSPSLDEI 674

RESULT 12
 0917F7 PRELIMINARY: PRT; 1373 AA.

AC 0917F7: 09V6K0: 024316;
 DT 01-MAR-2001 (TRENDEL); 16, Created
 DT 01-OCT-2001 (TRENDEL); 18, Last sequence update
 DE Tyrosine-protein kinase PR2 (EC 2.7.1.112).
 GN PR2 OR HD-11 OR G63969.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 NX Ephydriidae; Ephydriidae; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS);

RA STRAIN-BERKELEY;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E. Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner R., Henderson S.N.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Zhang Q., Chen L.X.,
 RA Balliu J.F., Abmayyan A., An H.-J., Andrews-Nelson C.R., Miklos G.L.G.,
 RA Beeson K.M., Basu P., Baxendale J., Bayraktoglu L., Beasly E.M.,
 RA Bortova D., Bortova M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burlingame K.C., Busam D.A., Butler H., Cadieu E., Cantler P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies A.,
 RA DePamphilis M., Delcher A., Deng Z., Dwyer D., Ewing R.,
 RA Durbin K.J., Evans R., Finkler R., Gage R., Gage R., Gage R.,
 RA Foster C., Gargiulo A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Harris N.L., Harvey D., Heiman T.D., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodali C.D., Kratz C., Kravitz J., Kuip D., Lai Z.,
 RA LaRoche P., Leiby T., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.F., McPherson D.,

RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Palazzo D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclet J.M.,
 RA Reinert K., Remington K., S. Pan S., Pollard J., Puri V., Reese M.G.,
 RA Shue B.C., Siden-Kiamos I., Saunders R.D.C., Scheeler F., Shen H.,
 RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
 RA Stryker R., Tector C., Turner R., Venter G.M., Weissbach J.,
 RA Wang Z.-Y., Wessarman D.A., Weinstein G.M., Wang A.H., Wang X.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu L.,
 RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C., Venter H.O.,
 RA "the genome sequence of Drosophila melanogaster";
 RA Science 287:2185-2195(2000).

SEQUENCE OF 13-777 FROM N.A. (LONG ISOFORM).
 RA STRAIN-OREGON-R; TISSUE=EMBRYO;
 RA MEDLINE-94156202; PubMed-8112607;
 RA Ito M., Matsui T., Taniguchi T., Chihara K.;
 RA "Alternative splicing generates two distinct transcripts for the
 RA Drosophila melanogaster fibroblast growth factor receptor homolog.";

SEQUENCE OF 266-321 FROM N.A.
 RA Oates A.C., Molberg P., Achon M.G., Wilks A.F.;
 RA "Sampling the genomic pool of protein tyrosine kinase genes using the
 RA polymerase chain reaction with genomic DNA";
 RA Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC TYROSINASE ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC -1- ALTERNATIVE PHOSPHATE.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING

RA EMBL: A6003819; AAF58423.2; ALT-SEQ.
 RA EMBL: D17551; BA004489.1; ALT-SEQ.
 RA HSSP: A0002909; CA005744.1; -;
 RA P1362; IFCG.
 RA FLYBASE: FBgn0013855; PR2.
 RA InterPro: IPR000719; Euk_pkinase.
 RA InterPro: IPR000095; PAKbox/RhoGing.
 RA InterPro: IPR001245; Ser_thr_pkinase.
 RA Pfam: PF00069; pkinase.
 RA PRINTS: PR00109; TYR_pkinase.
 RA PRODOM: PD000001; Euk_pkinase.
 RA SMART: SM00001; TYRKINASE.
 RA SMART: SM00285; PBD; 1.
 RA SMART: SM00220; S_TKC; 1.
 RA SMART: SM00219; TYRK; 1.
 RA PROSITE: P500107; PROTEIN KINASE ATP; 1.
 RA PROSITE: P50011; PROTEIN KINASE DOM; 1.
 RA TRANSFERASE: P500109; PROTEIN KINASE TYR; 1.
 RA ALTERNATIVE SPLICING: 1.
 RA DOMAIN: 133
 RA NP_BIND: 139 399
 RA BINDING: 147
 RA ACT_SITE: 164 164
 RA DOVAIN: 260 260
 RA VARSPLIC: 505 539
 RA FT: 82
 RA FT: 501
 RA FT: 769
 RA FT: 777

Query Match
 Best Local Similarity 9.8%; Score 130.5; DB 5; Length 1337;
 Matches 63; Conservative 34; Mismatches 103; Indels 59; Gaps 13;
 QY 1 MPKPTIYLKANKKGRKFKRLDILSPDILGDFHRTHTIKESQHDVEGDISL-59
 DB 462 LPSSTDFSEFVSQHSRISKRLR-----TMSKPNQNDPKHGVHIDGA--TEGDIATLG 515
 QY 60 -QGVNELLPGNKEAHGQPGHNEFRANSTDSVFTEP---SPVLKNAISLPFGGS 115
 DB 516 SSGYNNV-----KQIYVYKPSEDI-EQTPILLPTPTSPSLQTAGS- 559
 QY 116 QALMLPLSPVFN-----KQSFPAKLPRLSCPEVMEKAEKSSLENGTV-----HQ 167
 DB 560 -----TPPGANGSGAMGTSMNPTPTPSAEHTPLATVNGQSFPAQSTNPPPNK 612
 QY 168 GPTWSSGSSASQSGRSHSSLSLEQYPPADMDHPTPELTKIKKEESLSD- 227
 DB 613 GDDLE-FEGGHNYGADGKVSSET-----GM-----RPTSRIVDPHEHRTSD- 657
 QY 228 TGSLLSLDLDLPSILDEV 246
 DB 658 --EIAADKIDFSPSLDEI 674

Wed Apr 23 13:51:16 2003

us-09-806-276a-2.rsp

Db 479 LPBSTDSRSVSDHRSKRLR---TEMISKPNDFKHTGVCIDCA--TREGDIAFLG 532
OY 60 -OGNYELLPNGOKAHLQOPGNEFFRANSTSDVFTETP---SPVLKNAISLPTIGGS 115
Db 533 SSQYNNHVP-----KOIVTPYPSEDI-EGTPLLPTPTSPDSIQATSG- 576
OY 116 QALMLPLSPVTEGNS---KQESFPAKLPRLCEPVEEKAOKESLLNGVTV-----HQ 167
Db 577 -----YFEGANSOGAMGTSMNFTIPSAHEPTKILATNGOSDFASGNTNFFPR 629
OY 168 GDTSMGSSGASOGGRDSSSLSEQYPPMDPAEDMDHPTPCELIKGTKEESLSDL 227
Db 630 GDEL-ERGLNYGADGKSVHSET-----GM-----RPTSRIVDDPHETHEISD- 674
OY 228 TGSLSLQDLGSLDDEV 246
Db 675 --EIAADKIDFSPSLDEI 691

RESULT 13
PRELIMINARY: PRT: 150 AA.

090279 ID 090279: PRELIMINARY: PRT: 150 AA.
AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update) (Blinder of RHO
DE CRIB-containing BORG3 protein (201007002Rik)
DE GTPase 3).
CN BORG3 OR 201007002Rik.
OS Mus musculus (Mouse); Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE-EMBRYO;
RC MEDLINE-99421943; PubMed-10490598;
RX Joberty G., Perlungher R.R., Macara I.G.,
RT "The BORGs, a new family of Cdc42 and Tcl1 GTPase-interacting
RL proteins.", Mol. Cell. Biol. 19:6585-6597(1999).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Glasel C., King B., Kochava H.,
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Stabili F., Suzuki R., Aono H., Balderelli R., Barsi G.,
RA Sakai K., Oikio T., Furuno M., Carinacci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Kamya M., Lee N.H.,
RA Guellinich S., Hill D., Hofmann M., Mazzei L., Mombauts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzei L., Sakamoto N.,
RA Nodone P., Ring B., Ringwald M., Rodriguez T., Storch K.F.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Winding L.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Winkler S.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlsuhl S.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlsuhl S.,
RN Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.",
RN Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R., et al. (2001) to the EMBL/GenBank/DBD databases.
RL EMBL: AF164119; AAD48816.1;
DR EMBL: AK008154; BAB25498.1;
DR EMBL: BC006758; AA06758.1;
DR MGI:1929745; BORG3.

DR InterPro: IPR000095; PAKbox/Rhobdng.
DR SMART: SM00285; PBD: 1.
SQ SEQUENCE 150 AA; 15545 MW; 9AB9A49A9518B200 CRC64;
OY 9 4%: Score 124; DB 11; Length 150;
Best local similarity 23.2%; Pred. No. 0.00096;
Matches 57; Conservative 14; Mismatches 39; Indels 136; Gaps 10;
OY 9 LKANKKKEKELDLSPMISPLGDFRTHIGKEGQHDVFGDISPLGVELLPG 49
Db 4 MKOLGAPKPKRLDRLGALS--ISAPLDFRTHLHVGRG--DAGDLSFL 128
OY 69 NOEKAHIGOPGNEFFRANSTSDVFTETPSPYLKNAISLPTIGSQALMLPLSPYTE 128
Db 50 --SRHGSGPP-----PDP-----GAP-----PVAVP----- 68
OY 129 NSKQESFPAKLPRLCEPVEEKAOKESLLNGVTV-----HQ 83
Db 69 ---HSAVAPPAPO---PVAV----- 248
OY 189 SSSLSEQYPPMDPAEDMDHPTPCELIKGTKEESLSLQDLGSLDDEVIN 248
Db 84 -----PSPAD-----PLSFHLDLGPMSLDVAVLG 107

RESULT 14
PRELIMINARY: PRT: 150 AA.

0920X0 ID 0920X0: PRELIMINARY: PRT: 150 AA.
AC 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cdc42 effector protein 5.
CN BORG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-21125609; PubMed-11035016;
RX Hirsch D.S., Pirone D.M., Burdello P.D.,
RT "A New Family of Cdc42 Effector Proteins, CEPS, Function in Fibroblast
RL and Epithelial Cell Shape Changes.",
DR J. Biol. Chem. 276:875-883(2001).
DR EMBL: AF102773; AAD17906.1;
DR MGI:1929745; BORG3.
DR SMART: IPR000095; PAKbox/Rhobdng.
DR SMART: SM00285; PBD: 1.
SQ SEQUENCE 150 AA; 15630 MW; 8026AAD58CC8B200 CRC64;
OY 31 ISPLDGFRTTHIGKEGQHDVFGDISPLGVELLPGNOEKAHIGOPGNEFFRANST 57
Db 23 ISAPLDFRTHLHVGRG--DAGDLSFL-----SRHGSGPP----- 57
OY 91 SDSVFTETPSPYLKNAISLPTIGSQALMLPLSPYTEFNSKQESFPAKLPRLCEPVE 150
Db 58 -----PDP-----GAP-----PVAVP----- 68
OY 151 EKAQKSSLLNGVTVHOGDTSWSSGASQASQSGNDSSSLSEQYPPMDPAEDMDHPTP 210
Db 84 -----PSP 86
OY 211 CELINGKTKSEESLSLQDLGSLDDEVINVMK 254

OM protein - protein search, using SW INDC-
 April 23, 2003, 10:53:45 ; Search time 50.3484 seconds
 (without alignments)
 Run on: 619.298 Million cell updates/sec

US-09-806-276A-1

Sequence: 1 MEAPAQLLF LLDND...

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 1000000
-born parameters: 908470

Total number of months: 0

Minimum DB seq length: 2000000000
Maximum DB seq length: 2000000000

Post-processing:	Minimum	Maximum
	Match	Match
	100%	100%

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Database :
1: A_Geneseq_101002:*
   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

```

[illegible]

23: /SIBS2/90300000, 2

Description

Result No.	Score	Query Match	Length	DB	ID
1	112	100.0	234	21	AAV92239
2	113.5	93.5	235	21	AAV93702
3	113.5	93.5	235	21	AAV93729
4	113.1	93.3	234	21	AAV94066
5	112.7	93.0	234	21	AAV93708
6	112.7	93.0	234	21	AAV93733
7	111.6	92.1	236	22	AAV71272
8	111.6	92.1	236	23	ABG63490
9	114.5	92.0	233	21	AAV93704
10	114.5	92.0	233	21	AAV93731

11	1108	91.4	236	23	AAU74299
12	1098	90.6	236	23	AAU74301
13	1084	89.4	234	15	AAW52951
14	1073	88.5	234	12	AAW36608
15	1055.5	87.1	234	12	AAW31228
16	1055.5	87.1	239	12	AAW13111
17	1055.5	87.1	414	12	AAW13018
18	1053	86.9	238	19	AAW30304
19	1053	86.9	238	21	AAW14777
20	1053	86.9	238	21	AAW90927
21	1053	86.9	238	21	AAW74942
22	1053	86.9	238	19	AAW83031
23	1047	86.4	238	21	AAW14772
24	1047	86.4	238	21	AAW90922
25	1047	86.4	238	23	AAW74891
26	1047	86.4	238	23	AAW74937
27	1042.5	86.0	384	22	AAU14461
28	1042.5	86.0	384	22	AAU14463
29	1042.5	86.0	384	22	AAU14464
30	1042.5	86.0	384	22	AAU14465
31	1042.5	86.0	384	22	AAU14466
32	1042.5	86.0	384	22	AAU14467
33	1042.5	86.0	384	22	AAU14468
34	1042.5	86.0	384	22	AAU14469
35	1042.5	86.0	384	22	AAU14470
36	1042.5	86.0	384	22	AAU14471
37	1042.5	86.0	384	22	AAU14472
38	1042.5	86.0	384	22	AAU14473
39	1042.5	86.0	384	22	AAU14474
40	1042.5	86.0	384	22	AAU14475
41	1042.5	86.0	384	22	AAU14476
42	1042.5	86.0	384	22	AAU14477
43	1042.5	86.0	384	22	AAU14478
44	1042.5	86.0	384	22	AAU14479
45	1042.5	86.0	384	22	AAU14480

ALIGNMENTS

RESULT 1
AAV92239
Protein: 234 AA.

XX
LD
NAV92239:

10-ANG-2000 (first entry)

	bone marrow-derived serum protein 1.
10	10
20	20
30	30
40	40
50	50
60	60
70	70
80	80
90	90
100	100

DE Human donor serum protein; immunoglobulin kappa 1-3
XX narrow-derived serum protein; antithrombotic; antiasthmatic; antidiabetic; antiviral;

KM Bone marrow; anti-HIV; antiretroviral
KM BMDSP-1; cyostatic; anti-HIV; antiretroviral
KM BMDSP-1; cyostatic; anti-HIV; antiretroviral
KM BMDSP-1; cyostatic; anti-HIV; antiretroviral

anti-malarial
antiparasitic

XX
OS Homo sapiens.

	Location/Qualitiers
XX	II phosphorylation site
XX	kinase II
FH	Key

Feature	Location	Description
Modified site	10	potential casein
FT	11	/note= phosphorylation site
FT	12	kinase II

FT		34	"potential casein kinase"
FT	Modified-site	/note=	
nm		110	

Domain	36...110 /label= immunoglobulin_domain"
FT	
ET	

Modified-site	42	"potential protein kinase C phosphorylation site"
ET		
FT		

FT	72	"potential protein kinase C site"
Modified-site	/note=	
FT		ri phosphorylation site"

FT	87	potential casein kinase II phospho-
FT	Modified-site	ri phosphorylation site
FT	/note=	

FT	Modified site	96
FT	/note= "potential casein kinase II phospho-	

FT	FT	Modified-site
FT	FT	Modified-site

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FT FT Domain /note="potential casein kinase II phosphorylation site"
FT FT 147..216 /label="immunoglobulin_domain"
FT FT Domain 151..173 /label="signature_sequence"
FT FT Modified-site /note="immunoglobulin"
FT FT Modified-site 182 /note="potential casein kinase II phosphorylation site"
FT FT Modified-site 184 /note="potential casein kinase II phosphorylation site"
FT FT Domain 190..233 /label="signature_sequence"
FT FT Modified-site 202 /note="immunoglobulin"
FT FT Domain /note="potential casein kinase II phosphorylation site"
FT FT 212..229 /label="signature_sequence"
FT FT /note="immunoglobulin"
PD PD W0200020588-A2.
XX XX 13-APR-2000.
PF PF 01-OCT-1999; 99WO-US22908.
XX XX 02-OCT-1998; 98US-0165621.
XX XX (INCY-) INCYTE PHARM INC.
XX XX Tang YT, Corley NC, Guegler KU, Lu DM;
DR DR WPI: 2000-303775/26.
XX XX N-PSDB: AAA09154.
PT PT Purified polypeptide for treating or preventing disorders associated
PT PT with decreased expression or activity of bone marrow-derived serum
PS PS proteins
XX XX Claim 1; Page 68-69; 72pp; English.
CC CC Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and
CC CC structural similarity with immunoglobulin kappa light chain. BMDSP-1
CC CC and BMDSP-2 are useful for treating or preventing a disorder associated
CC CC with decreased expression or activity of bone marrow-derived serum
CC CC Antagonists of BMDSP are useful for treating or preventing a disorder associated
CC CC associated with increased expression or activity of BMDSP.
CC CC serum proteins. The disorders include cancer (melanoma, adenocarcinoma,
CC CC sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
CC CC asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
CC CC (schistosoma, tapeworm), viral infections, parasitic infections,
CC CC hypertension, vasculitis), and vascular disorders (arteriosclerosis,
SQ SQ Sequence 234 AA:
Query Match
Best Local Similarity 100.0%; Score 1212; DB 21; Length 234;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEMPALFLLLMLPDTTGEIVLTQSPATLSISGERATLSCAASQSVSYLAWYQOR 60
DB 1 MEMPALFLLLMLPDTTGEIVLTQSPATLSISGERATLSCAASQSVSYLAWYQOR 60
OY 61 GOAPRLIYDASNRATGIPRRSGSGSDFTLTISLREDEVALYCCQYFTPTPTG 120
DB 61 GOAPRLIYDASNRATGIPRRSGSGSDFTLTISLREDEVALYCCQYFTPTPTG 120
OY 121 GTRLEIKRTVAAPSVFIFPPSDEQLKGTASVYCLNNFYPREAKVQWKVDNALQSGNS 180
DB 121 GTRLEIKRTVAAPSVFIFPPSDEQLKGTASVYCLNNFYPREAKVQWKVDNALQSGNS 180
OY 181 ESYTQDSKDSSTYSILSTLTLSKADYEKKRYACEVTHQGLSSPVTKSPNRGEC 234
DB 181 ESYTQDSKDSSTYSILSTLTLSKADYEKKRYACEVTHQGLSSPVTKSPNRGEC 234

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DB 181 ESYTQDSKDSSTYSILSTLTLSKADYEKKRYACEVTHQGLSSPVTKSPNRGEC 234
RESULT 2
ID AAY93702
XX AAY93702 standard; Protein; 235 AA.
AC AAY93702;
XX 03-OCT-2000 (first entry)
DE The kappa chain of immunoglobulin clone 4.1.1.
XX KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX KW Proliferative disorder; cancer; immunodeficient disorder.
OS Homo sapiens.
XX W0200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US30895.
XX 23-DEC-1998; 98US-0113647.
XX (PFI2) PFIZER INC.
XX (ABGE-) ABERNETHY INC.
XX Hanson DC, Neuven MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvatan JR;
XX WPI: 2000-442647/38.
XX N-PSDB: AAA6865.
PT PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT PT (CTLA-4) containing specified heavy and light chain sequences, useful
PS PS for treating, e.g. immune disorders
XX XX Claim 3; Fig 1A; 157pp; English.
CC CC The present sequence represents a kappa chain of an antibody of the
CC CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC CC FRI-FR3 sequence, comprising a modified conglutinin sequence from a
CC CC modification encoded by a human VH3-33 family gene. The
CC CC The antibodies may be used to inhibit CTLA-4 and/or framework regions.
CC CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC CC disease, diabetes and graft rejection) and proliferative disorders
CC CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC CC immune system to up-regulate immunodeficient disorders.
SQ SQ Sequence 235 AA:
Query Match
Best Local Similarity 93.5%; Score 1133.5; DB 21; Length 235;
Matches 219; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
OY 1 MEMPALFLLLMLPDTTGEIVLTQSPATLSISGERATLSCAASQSVSYLAWYQOR 60
DB 1 MEMPALFLLLMLPDTTGEIVLTQSPATLSISGERATLSCAASQSVSYLAWYQOR 60
OY 60 GOAPRLIYDASNRATGIPRRSGSGSDFTLTISLREDEVALYCCQYFTPTPTG 119
DB 60 GOAPRLIYDASNRATGIPRRSGSGSDFTLTISLREDEVALYCCQYFTPTPTG 119
OY 120 GTRLEIKRTVAAPSVFIFPPSDEQLKGTASVYCLNNFYPREAKVQWKVDNALQSGNS 179
DB 120 GTRLEIKRTVAAPSVFIFPPSDEQLKGTASVYCLNNFYPREAKVQWKVDNALQSGNS 179
OY 180 ESYTQDSKDSSTYSILSTLTLSKADYEKKRYACEVTHQGLSSPVTKSPNRGEC 234
DB 180 ESYTQDSKDSSTYSILSTLTLSKADYEKKRYACEVTHQGLSSPVTKSPNRGEC 234

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DB 181 QESVTEQDSKDSYSLSTLTLSKADYEKKHYACETVHQGLSSPYTKSPNRGEC 235

RESULT 3
AAV93729
ID AAV93729 standard; Protein; 235 AA.

XX AAV93729;

AC 03-OCT-2000 (first entry)

XX The kappa chain of immunoglobulin clone 4.1.1.

DE Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

FT Key Location/Qualifiers
FT Peptide 1..20
/note="signal peptide"

XX MO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US30895.

XX 23-DEC-1998; 98US-0113647.

XX (PRIZ) PEIZER INC.
XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG;
PI Corvatan JR;

XX WPI: 2000-442647/38.
XX N-PSDB; AAA46893.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders -

XX Claim 3; Fig 22g; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FRI sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.

XX Sequence 235 AA;

Query Match 93.5%; Score 1133.5; DB 21; Length 235;
Best Local Similarity 93.2%; Pred. No. 3.8e-62;
Matches 219; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

OY 1 MEAPQQLFLILLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASGV-SSYLAWYQOK 59
DB 1 MEAPQQLFLILLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASGV-SSYLAWYQOK 60
OY 60 PQAPRLIYDASNATGIPRFGSGSGTDTLTISLLEPDVALYCCQGYFTTPTFFG 119
DB 61 PQAPRLIYDASNATGIPRFGSGSGTDTLTISLLEPDVALYCCQGYFTTPTFFG 120

OY 120 QSTRLEIKRTVAAPSVFIFPPSDEQKSGTASVCLLNNFIPREAKVKYDNLQSGNS 179
DB 121 QSTRLEIKRTVAAPSVFIFPPSDEQKSGTASVCLLNNFIPREAKVKYDNLQSGNS 180

OY 180 QESVTEQDSKDSYSLSTLTLSKADYEKKHYACETVHQGLSSPYTKSPNRGEC 234
DB 181 QESVTEQDSKDSYSLSTLTLSKADYEKKHYACETVHQGLSSPYTKSPNRGEC 235

RESULT 4

AA014066
ID AA014066 standard; Protein; 234 AA.

XX AA014066;

AC 07-MAY-2002 (first entry)

XX Light chain protein of the monoclonal antibody from clone JA.

DE HRIQ; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW light chain; central nervous system; CNS; prophylactic therapy; clone JA.

XX Homo sapiens.

XX WO200188132-A2.

XX 22-NOV-2001.

XX 04-MAY-2001; 2001WO-US14468.

XX 16-MAY-2000; 2000US-204518P.

XX (UYUE-) UNIV JEFFERSON THOMAS.

XX Hooper DC, Dietzschold B;

XX WPI: 2002-062381/08.
XX N-PSDB; AAK98702.

XX Novel isolated human monoclonal rabies virus neutralising antibody
PT useful for treating individual exposed to rabies virus and for
PT preventing spread of rabies virus to central nervous system -

XX Claim 4; Page 24-25; 25pp; English.

XX This sequence represents the light chain protein of the monoclonal
CC antibody from clone JA. The invention relates to an isolated human
CC monoclonal rabies virus neutralising antibody (virucide) derived from
CC cDNA clones encoding the antibody heavy and light chains expressed in
CC heterologous expression systems and purified away from deleterious
CC contaminants. The invention provides a fused gene encoding a chimeric
CC immunoglobulin light chain and a fused gene encoding a chimeric
CC immunoglobulin heavy chain. The antibody of the invention is useful for
CC treating an individual exposed to a rabies virus by administering to the
CC individual a therapeutically effective amount of the antibody, and
CC preventing a spread of the rabies virus to the central nervous system
CC (CNS). The antibody of the invention provides a safe and efficacious post
CC -exposure prophylactic therapy for individuals exposed to a rabies virus.

XX Sequence 234 AA;

Query Match 93.3%; Score 1131; DB 23; Length 234;
Best Local Similarity 92.7%; Pred. No. 5.4e-62;
Matches 217; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 MEAPQQLFLILLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASGVSSYLAWYQOK 60
DB 1 MEAPQQLFLILLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASGVSSYLAWYQOK 60
OY 61 GOAPRLIYDASNATGIPRFGSGSGTDTLTISLLEPDVALYCCQGYFTTPTFFG 120
DB 61 GOAPRLIYDASNATGIPRFGSGSGTDTLTISLLEPDVALYCCQGYFTTPTFFG 120

OY 121 GTRLEIKRTVAAPSVFIPEPPSDEQLKSGTASVYCLLNFFYPREAKYQKVDNALQSGNSQ 180
 DB 121 GTRLEIKRTVAAPSVFIPEPPSDEQLKSGTASVYCLLNFFYPREAKYQKVDNALQSGNSQ 180
 OY 181 ESYTEODSKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 234
 DB 181 ESYTEODSKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 5
 AAY93708
 ID AAY93708 standard; Protein: 234 AA.
 AC AAY93708;
 DT 03-OCT-2000 (first entry)
 DE The kappa chain of immunoglobulin clone 6.1.1.
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.
 OS Homo sapiens.
 PN MO200037504-A2.
 PD 29-JUN-2000.
 PF 23-DEC-1999; 99WO-US30895.
 PR 23-DEC-1998; 98US-0113647.
 PA (PF12) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 DR WPI: 2000-442647/38.
 DR N-PSDB; AAA46871.
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 PS Claim 3; Fig 1D; 157pp; English.

CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

SO Sequence 234 AA;
 Query Match 93.0%; Score 1127; DB 21; Length 234;
 Best Local Similarity 92.7%; Pred. No. 9.5e-62;
 Matches 217; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 MEAPQQLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKP 60
 DB 1 MEAPQQLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKP 60
 OY 61 GOAPRLIYDASNRATGIPPRFSSGSGCTDFTLTLSRLEPEDVALYYCOQYFTPTPTFGQ 120
 DB 61 GOAPRLIYDASNRATGIPPRFSSGSGCTDFTLTLSRLEPEDVALYYCOQYFTPTPTFGQ 120

DB 61 GOAPRLIYDASNRATGIPPRFSSGSGCTDFTLTLSRLEPEDVALYYCOQYFTPTPTFGQ 120
 OY 121 GTRLEIKRTVAAPSVFIPEPPSDEQLKSGTASVYCLLNFFYPREAKYQKVDNALQSGNSQ 180
 DB 121 GTRLEIKRTVAAPSVFIPEPPSDEQLKSGTASVYCLLNFFYPREAKYQKVDNALQSGNSQ 180
 OY 181 ESYTEODSKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 234
 DB 181 ESYTEODSKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 6
 AAY93733
 ID AAY93733 standard; Protein: 234 AA.
 AC AAY93733;
 DT 03-OCT-2000 (first entry)
 DE The kappa chain of immunoglobulin clone 6.1.1.
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KM proliferative disorder; cancer; immunodeficient disorder.
 OS Homo sapiens.
 PN MO200037504-A2.
 PD 29-JUN-2000.
 PF 23-DEC-1999; 99WO-US30895.
 PR 23-DEC-1998; 98US-0113647.
 PA (PF12) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 DR WPI: 2000-442647/38.
 DR N-PSDB; AAA46897.
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 PS Claim 3; Fig 22c; 157pp; English.

CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

SO Sequence 234 AA;
 Query Match 93.0%; Score 1127; DB 21; Length 234;
 Best Local Similarity 92.7%; Pred. No. 9.5e-62;
 Matches 217; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 MEAPQQLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKP 60
 DB 1 MEAPQQLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKP 60

XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Haseltine WA;
 PI WPI; 2002-010886/01.

DR New fusion protein for treating disease e.g. diabetes comprises an
 XX albumin fused to a therapeutic protein -
 PT Claim 1; Page 682; 2102pp; English.
 PS

CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. Alzheimer's, hematopoietic disorders, neural disorders
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
 CC fusion proteins of the invention.

CC Sequence 236 AA;

Query Match 92.1%; Score 1116; DB 23; Length 236;
 Best Local Similarity 92.8%; Pred. No. 4.5e-61;

Matches 219; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 MEAPQQLFLLLMLPDTTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAAYQOKP 60
 DB 1 MEXPAQLFLLLMLPDTTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAAYQOKP 60
 QY 61 GOAPRLILYDASNRATGIPRPSGSGSGTDTLTLSLEPEDVALYCCQYFTTP--YTF 118
 DB 61 GOAPRLILYDASNRATGIPRPSGSGSGTDTLTLSLEPEDVALYCCQYFTTP--YTF 120
 QY 119 GGGIRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGN 178
 DB 121 GGGIRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGN 180
 QY 179 SOESTEDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
 DB 181 SOESTEDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 9

AA93704
 ID AAY93704 standard; Protein; 233 AA.

AC AAY93704;

DT 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.8.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

PN WO200037504-A2.

PD 29-JUN-2000.

PF 23-DEC-1999; 99WO-US30895.

PR 23-DEC-1998; 98US-0113647.

XX (Pfizer) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvatan JR;
 DR WPI; 2000-442647/38.
 DR N-PSDB; AAA46867.

CC Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 CC (CTLA)-4 containing specified heavy and light chain sequences, useful
 CC for treating, e.g. immune disorders -
 CC Claim 3; Fig 1B; 157pp; English.

CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.

CC Sequence 233 AA;

Query Match 92.0%; Score 1114.5; DB 21; Length 233;
 Best Local Similarity 92.7%; Pred. No. 5.5e-61;

Matches 217; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MEAPQQLFLLLMLPDTTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAAYQOKP 60
 DB 1 MEXPAQLFLLLMLPDTTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAAYQOKP 59
 QY 61 GOAPRLILYDASNRATGIPRPSGSGSGTDTLTLSLEPEDVALYCCQYFTTPYTFQ 120
 DB 60 GOAPRLILYDASNRATGIPRPSGSGSGTDTLTLSLEPEDVALYCCQYFTTPYTFQ 119
 QY 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGN 180
 DB 120 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGN 179
 QY 181 ESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
 DB 180 ESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 10

AA93731
 ID AAY93731 standard; Protein; 233 AA.

AC AAY93731;

DT 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.8.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

PN WO200037504-A2.

PF Key Location/Qualifiers
 FT Peptide 1..20
 FT /note="signal peptide"

PN 23-DEC-1999; 99WO-US30895.

PD 29-JUN-2000.
 XX 23-DEC-1999; 99WO-US30895.
 XX 23-DEC-1998; 98US-0113647.
 PR (PFIZ.) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 PI Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG;
 PI Corvahan JR;
 DR WPI: 2000-442647/38.
 XX N-PSDB: AAA46895.
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 3; Fig 22k; 157pp; English.
 CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 XX Sequence 233 AA;
 SQ
 Query Match 92.0%; Score 1114.5; DB 21; Length 233;
 Best Local Similarity 92.7%; Pred. No. 5.5e-61;
 Matches 217; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 QY 1 MEAPQALLFLLLMLPPTGGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKP 60
 DB 1 METPAQLFLLLMLPPTGGEIVLTQSPGTLSPGERATLSCRTSVS-SYLAWYQOKP 59
 QY 61 GOAPRLLIYDASNRATGIPRFGSGSGTDTLTISRLEPEDVALYYCOQYFTTPYTF 120
 DB 60 GOAPRLLIYDASNRATGIPRFGSGSGTDTLTISRLEPEDVALYYCOQYFTTPYTF 119
 QY 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWKVDNALQSGNSQ 180
 DB 120 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWKVDNALQSGNSQ 179
 QY 181 ESVTEDSDKSTYSLSTLTLSKADYEKHKYACEVTHQGLSPVTKSFNRGEC 234
 DB 180 ESVTEDSDKSTYSLSTLTLSKADYEKHKYACEVTHQGLSPVTKSFNRGEC 233
 RESULT 11
 AAU74299
 ID AAU74299 standard; Protein; 236 AA.
 XX AAU74299;
 AC
 XX 12-MAR-2002 (first entry)
 DE Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
 XX
 XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;

KW systemic lupus erythematosus; autoimmune disorder; inflammation;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 OS Homo sapiens.
 XX WO200187981-A2.
 PN 22-NOV-2001.
 XX 15-MAY-2001; 2001WO-JP04035.
 PF 18-MAY-2000; 2000JP-0147116.
 PR 30-MAR-2001; 2001JP-0099508.
 XX (NISB) JAPAN TOBACCO INC.
 PA Tsuji T, Tezuka K, Hori N;
 PI WPI: 2002-075313/10.
 DR N-PSDB: AAS9475.
 XX
 PT New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation -
 XX
 PS Claim 30; Page 284-285; 300pp; English.
 CC The invention relates to a novel human antibody (1), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AILIM). (1) is useful for modulating signal
 CC transduction into a cell mediated by AILIM, for modulating proliferation
 CC of AILIM-expressing cells, for modulating production of a cytokine from
 CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AILIM-expressing cells. (1) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (1) is useful for treating and
 CC preventing various diseases associated with AILIM-mediated
 CC costimulatory transduction, and for inhibiting the onset and/or
 CC advancement of the diseases. (1) is useful for suppression,
 CC prevention and/or treatment of rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, allergic lupus erythematosus,
 CC chronic inflammatory dermatosis, systemic lupus erythematosus, or allergic
 CC insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic
 CC disorders, inflammation, graft versus host reaction, graft versus host
 CC disease, immune rejection, disorders caused by abnormal intestinal
 CC immunity, specifically inflammatory intestinal disorders such as
 CC ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and
 CC pancreatitis. (1) induces no serious immunorejection due to antigenicity
 CC to human, i.e., human anti-mouse antigenicity (HMA) in a host.
 CC AAU74296-AAU74301 represent anti-human AILIM monoclonal antibody amino
 CC acid sequences of the invention.
 XX
 SQ Sequence 236 AA;
 Query Match 91.4%; Score 1108; DB 23; Length 236;
 Best Local Similarity 91.9%; Pred. No. 1.4e-60;
 Matches 217; Conservative 9; Mismatches 8; Indels 2; Gaps 2;
 QY 1 MEAPQALLFLLLMLPPTGGEIVLTQSPATLSLSPGERATLSCRASQSV-SYLAWYQOK 59
 DB 1 METPAQLFLLLMLPPTGGEIVLTQSPGTLSPGERATLSCRTSVS-SYLAWYQOK 60
 QY 60 PGQAPRLLIYDASNRATGIPRFGSGSGTDTLTISRLEPEDVALYYCOQYFTTPY-TF 118
 DB 61 PGQAPRLLIYDASNRATGIPRFGSGSGTDTLTISRLEPEDVALYYCOQYFTTPY-TF 120
 QY 119 GOGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWKVDNALQSGN 178
 DB 121 GOGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKYQWKVDNALQSGN 180
 QY 179 SOESVTEDSDKSTYSLSTLTLSKADYEKHKYACEVTHQGLSPVTKSFNRGEC 234
 DB 180 SOESVTEDSDKSTYSLSTLTLSKADYEKHKYACEVTHQGLSPVTKSFNRGEC 233

DB 181 SOESVTEODSKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 236

RESULT 12

AAU74301

AAU74301 standard; Protein: 236 AA.

12-MAR-2002 (first entry)

Anti-human ALLM monoclonal antibody clone Jmab-139, light chain.

Human: antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antitumor; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; ALLM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic lupus erythematosus; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammatory; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

Homo sapiens.

WO200187981-A2.

22-NOV-2001.

15-MAY-2001: 2001WO-JP04035.

18-MAY-2000: 2000JP-0147116.

30-MAR-2001: 2001JP-0099508.

(NIBS) JAPAN TOBACCO INC.

Tsuji T, Tezuka K, Hori N;

WPI: 2002-075313/10.

N-PSDB; AAS99477.

New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation

Claim 30: Page 298-299; 300pp; English.

The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte transduction into a cell mediated by ALLM, for modulating proliferation of ALLM-expressing cells, for modulating production of a cytokine from ALLM-expressing cells, and for inducing antibody-dependent cytotoxicity against ALLM-expressing cells and/or immune cytotoxicity or apoptosis of ALLM-expressing cells. (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with ALLM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppressing, preventing and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection disorders caused by abnormal intestinal ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (I) induces no serious immunorejection due to antigenicity to human, i.e., human anti-mouse immunoreactivity (HAMA) in a host. AAU74296-AAU74301 represent anti-human ALLM monoclonal antibody amino acid sequences of the invention.

SO Sequence 236 AA;

Query Match

Best Local Similarity 90.6%; Score 1098; DB 23; Length 236; Matches 216; Conservative 9; Mismatches 9; Indels 2; Gaps 2;

QY 1 MEAPAQLEFLLLMLPDTGEIVYVTSPTATSLSPERATLSRASQSV-SSTLAWYQOK 59

Db 1 MEPAQLLEFLLLMLPDTGEIVYVTSPTATSLSPERATLSRASQSV-SSTLAWYQOK 60

QY 60 PGAPRLIYDASNRATGIPRFGSGSGTDFLTITSLRLEPEVVALYCGQYFTPY-TF 118

Db 61 PGAPRLIYDASNRATGIPRFGSGSGTDFLTITSLRLEPEVVALYCGQYFTPY-TF 120

QY 119 GCGTRLEIKRTVAAPSVFIFPPSDEQKSGTASVCLLNNFPRAKYQMKVDNALQSGN 178

Db 121 GCGTRLEIKRTVAAPSVFIFPPSDEQKSGTASVCLLNNFPRAKYQMKVDNALQSGN 180

QY 179 SOESVTEODSKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 234

Db 181 SOESVTEODSKDSTVSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 236

RESULT 13

AAU74301

AAU74301 standard; Protein: 234 AA.

27-OCT-1994 (first entry)

Human anti-IgE Mab light chain.

Human IgE: CH4 region; triggers mediator release; Mast cells; Monoclonal antibody; allergy.

Homo sapiens.

Key Location/Qualifiers

Region 21..128 /label= light chain variable region

EP592230-A.

13-APR-1994.

07-OCT-1993: 93EP-0308006.

07-OCT-1992: 92JP-0293800.

(SNOW) SNOW BRAND MILK PROD CO LTD.

Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;

Yoshida T;

WPI: 1994-120330/15.

N-PSDB; AAQ71872.

Human monoclonal anti-IgE peptide antibody - inhibits histamine release from mast cells by allergen stimulation, useful for preventing allergies

Claim 3; Page 12; 21pp; English.

AAU74296 shows the light chain of a human type anti-IgE peptide monoclonal antibody which inhibits the signal transduction for the release of chemical mediator from mast cells and basophils stimulated with allergen. The antibody can be used for the prophylaxis and the therapy of allergy.

Sequence 234 AA;

Query Match

89.4%; Score 1084; DB 15; Length 234;

Wed Apr 23 13:51:07 2003

us-09-806-276a-1.rag

CC able to pass across the placenta.
CC See also AAQ11879 and AAQ11880.
xx
SQ Sequence 349 AA;

Query Match (87.1%) Score 1055.5; DB 12; Length 349;
Best Local Similarity 63.0%; Pred. No. 3.2e-57;
Matches 220; Conservative 4; Mismatches 10; Indels 115; Gaps 2;

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OY 1 MEAPQALLFLMLPDTTGEIVLTOSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRPL 180
Db 1 MEAPQALLFLMLPDTTGEIVLTOSPATLSLSPGERATLSCRASQSVSYLAWYQOKP 60
OY 61 GQAPRLLIYDASNRAATGIPARFSGSGGTDFTLTISLEPEDFAVYCOHRDNMPGATF 109
Db 61 GQAPRPLIYDASNRAATGIPARFSGSGGTDFTLTISLEPEDFAVYCOHRDNMPGATF 120
OY 110 -----
Db 121 GGGTKVEIKHTTGEIVLTOSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRPL 180
OY 110 -----
Db 181 IYDASNRAATGIPARFSGSGGTDFTLTISLEPEDFAVYCOHRDNMPGATF 125
OY 126 IKRTVAPSVETIEPPSDQLKSGTASVYCLNNFYPREAKVOKVDNALQSGNSQESVTE 240
Db 241 IKRTVAPSVETIEPPSDQLKSGTASVYCLNNFYPREAKVOKVDNALQSGNSQESVTE 185
OY 186 ODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
Db 301 ODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 349
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Search completed: April 23, 2003, 11:01:06
Job time : 52.3484 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 10:59:20 ; Search time 12.4672 Seconds
(without alignments)
552.246 Million cell updates/sec

Title: US-09-806-276a-1

Perfect score: 1212
Sequence: 1 MERRYLLELLLELLLPDTTG.....EVTHQGLSSPVTSFNRGEC 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:.*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:.*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:.*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:.*
5: /cgn2.6/ptodata/1/1aa/PCRTUS.COMB.pep:.*
6: /cgn2.6/ptodata/1/1aa/backfilled1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	88.5	234	4	US-09-049-672A-6 Sequence 6, Appl 1
2	1009.5	83.3	235	1	US-08-276-852-153 Sequence 153, App
3	1009.5	83.3	235	1	US-08-899-575-153 Sequence 153, App
4	1009.5	83.3	235	1	US-08-899-575-153 Sequence 153, App
5	1009.5	83.3	235	5	PCR-US95-08743-153 Sequence 16, Appl 1
6	1003	82.6	235	5	US-08-812-586-16 Sequence 36, Appl 1
7	1001	82.1	240	4	US-09-301-593-36 Sequence 56, Appl 1
8	994.5	82.1	241	2	US-07-916-098A-56 Sequence 11, Appl 1
9	979.5	80.8	214	3	US-09-041-889-11 Sequence 6, Appl 1
10	979.5	80.8	214	3	US-08-837-058-11 Sequence 6, Appl 1
11	979.5	80.8	214	3	US-08-837-058-11 Sequence 6, Appl 1
12	968.5	79.9	239	3	US-08-480-753-8 Sequence 28, Appl 1
13	968.5	79.9	239	3	US-08-480-753-8 Sequence 28, Appl 1
14	961	79.3	240	4	US-09-301-593-28 Sequence 5, Appl 1
15	958	79.0	236	1	US-08-485-737B-69 Sequence 69, Appl 1
16	955.5	78.8	239	4	US-09-485-737B-69 Sequence 29, Appl 1
17	951.5	78.5	233	4	US-08-812-586-29 Sequence 97, Appl 1
18	947.5	78.2	235	4	US-09-111-945-97 Sequence 1, Appl 1
19	943	77.8	214	4	US-09-679-397-1 Sequence 25, Appl 1
20	943	77.8	214	4	US-09-680-148-1 Sequence 25, Appl 1
21	943	77.8	237	2	US-08-463-587A-25 Sequence 3, Appl 1
22	943	77.8	237	2	US-08-463-587A-25 Sequence 3, Appl 1
23	943	77.8	237	2	US-08-463-587A-25 Sequence 25, Appl 1
24	943	77.8	237	2	US-08-463-587A-25 Sequence 25, Appl 1
25	941	77.6	218	3	PCR-US91-09133-26 Sequence 13, Appl 1
26	941	77.6	218	3	US-08-887-352B-13 Sequence 9, Appl 1
27	941	77.6	218	4	US-09-109-207C-13 Sequence 13, Appl 1

28	941	77.6	218	4	US-09-296-005-13 Sequence 13, Appl 1
29	941	77.6	218	4	US-08-466-163B-9 Sequence 80, Appl 1
30	939	77.5	232	4	US-08-704-744-80 Sequence 2, Appl 1
31	938	77.4	218	5	PCR-US96-13152-2 Sequence 25, Appl 1
32	936.5	77.3	233	2	US-07-934-373C-2 Sequence 25, Appl 1
33	936.5	77.3	233	2	US-08-437-642B-25 Sequence 25, Appl 1
34	936.5	77.3	233	4	US-08-146-206C-25 Sequence 25, Appl 1
35	936.5	77.3	233	5	PCR-US93-07832-25 Sequence 4, Appl 1
36	935	77.1	214	4	US-09-247-352-4 Sequence 15, Appl 1
37	935	77.1	214	4	US-09-466-635-4 Sequence 15, Appl 1
38	934	77.1	218	2	US-08-887-352B-15 Sequence 19, Appl 1
39	934	77.1	218	2	US-08-887-352B-17 Sequence 19, Appl 1
40	934	77.1	218	2	US-08-887-352B-19 Sequence 19, Appl 1
41	934	77.1	218	2	US-08-887-352B-24 Sequence 15, Appl 1
42	934	77.1	218	4	US-09-109-207C-15 Sequence 17, Appl 1
43	934	77.1	218	4	US-09-109-207C-17 Sequence 19, Appl 1
44	934	77.1	218	4	US-09-109-207C-19 Sequence 24, Appl 1
45	934	77.1	218	4	US-09-109-207C-24 Sequence 24, Appl 1

ALIGNMENTS

RESULT 1
US-09-049-672A-6
Sequence 6, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Yang, Janice

APPLICANT: Cortley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HERMITH

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerione, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 234 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: COLSUCT01

CLONE: 2280869
US-09-049-672A-6

Query Match 88.5%; Score 1073; DB 4; Length 234;
Best Local Similarity 88.0%; Pred. No. 4e-80;
Matches 206; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEAPQQLFLILLMLPDTTGEIVLTOSPAFLISPERATLSCRASQSVSSYLAMYQOKP 60
DB 1 MEAPQQLFLILLMLPDTTGEIVLTOSPAFLISPERATLSCRASQSVSSYLAMYQOKP 60
QY 61 GOAPRLIITYASNRAGIIPRFGSGSGTDFLTITSRLEPEDVALYCOQYFTTPTTFFG 120
DB 61 GOAPRLIITYASNRAGIIPRFGSGSGTDFLTITSRLEPEDVALYCOQYFTTPTTFFG 120
QY 121 GTLEIKRRTVAAPSVFIIPPSPDEQLKSGTASVYCLNNFYPRKAVOMKVDNALQSGNSQ 180
DB 121 GTLEIKRRTVAAPSVFIIPPSPDEQLKSGTASVYCLNNFYPRKAVOMKVDNALQSGNSQ 180
QY 181 ESYTEDSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPYTKSFNRGEC 234
DB 181 ESYTEDSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPYTKSFNRGEC 234

RESULT 2

US-08-276-852-153
Sequence 153, Application US/08276852
Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-276-852-153

Query Match 83.3%; Score 1009.5; DB 1; Length 235;
Best Local Similarity 84.3%; Pred. No. 5.8e-75;
Matches 198; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEAPQQLFLILLMLPDTTGEIVLTOSPAFLISPERATLSCRASQSVSSYLAMYQOKP 59
DB 1 MEAPQQLFLILLMLPDTTGEIVLTOSPAFLISPERATLSCRASQSVSSYLAMYQOKP 59
QY 60 GOAPRLIITYASNRAGIIPRFGSGSGTDFLTITSRLEPEDVALYCOQYFTTPTTFFG 119
DB 60 GOAPRLIITYASNRAGIIPRFGSGSGTDFLTITSRLEPEDVALYCOQYFTTPTTFFG 119
QY 120 GTLEIKRRTVAAPSVFIIPPSPDEQLKSGTASVYCLNNFYPRKAVOMKVDNALQSGNS 179
DB 120 GTLEIKRRTVAAPSVFIIPPSPDEQLKSGTASVYCLNNFYPRKAVOMKVDNALQSGNS 179
QY 180 QESTVEDSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPYTKSFNRGEC 234
DB 180 QESTVEDSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPYTKSFNRGEC 234

RESULT 3

US-08-899-575-153
Sequence 153, Application US/08899575
Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-899-575-153

US-08-899-575-153

; Sequence 16, App

US-08-012 300
; Sequence 16, Application US/0881258

Patent No. 6048704
 GENERAL INFORMATION:
 APPLICANT: Martin David Tilson
 TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABOINTEL AORTIC ANEURYSM (AAA)
 NUMBER OF INVENTION: DISSEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
 CORRESPONDENCE ADDRESS:
 ADDRESS: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/812,586
 FILING DATE: 07-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-812-586-16

Query Match
 Best Local Similarity 82.8%; Score 1003; DB 3; Length 235;
 Matches 197; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 MEAPQALLFLMLPDTGEIVLTQSPATLSLSPGERATLSCRASQSY-----SYLA 54
 Db 3 MEAPQALLFLMLPDTGEIVLTQSPATLSLSPGERATLSCRASQSY-----SYLA 54
 QY 61 GAAPRLIYDASNRATGIPRFSGSGGTDFLTLSLPEDEVALYVCOQYFTT 114
 Db 63 GAAPRLIYDASNRATGIPRFSGSGGTDFLTLSLPEDEVALYVCOQYFTT 114
 QY 121 GTRLEIKRTVAASVFIPEPSDEQLKSGTASVYCLLNFFPREAKYQMKVDNALQSGNSQ 180
 Db 123 GTRLEIKRTVAASVFIPEPSDEQLKSGTASVYCLLNFFPREAKYQMKVDNALQSGNSQ 180
 QY 181 ESYVEDQSKDSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 183 ESYVEDQSKDSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 7
 US-09-301-593-36
 Sequence 36, Application US/09301593A
 Patent No. 6455677
 GENERAL INFORMATION:
 APPLICANT: Park, John E.
 APPLICANT: Garin-Chesa, Pilar
 APPLICANT: Bamberg, Uwe
 APPLICANT: Leger, Olivier
 APPLICANT: Saldanha, Jose W.
 APPLICANT: Rettig, Wolfgang J.
 TITLE OF INVENTION: FAB-Specific Antibody with Improved Productibility
 FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A
 CURRENT FILING DATE: 1999-04-29
 EARLIER APPLICATION NUMBER: EP 98107925.4
 EARLIER FILING DATE: 1998-04-30
 EARLIER APPLICATION NUMBER: US 60/086,049
 NUMBER OF SEQ ID NOS: 108
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 36
 LENGTH: 240
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-301-593-36

Query Match
 Best Local Similarity 79.6%; Score 1001; DB 4; Length 240;
 Matches 191; Conservative 25; Mismatches 18; Indels 6; Gaps 1;

QY 1 MEAPQALLFLMLPDTGEIVLTQSPATLSLSPGERATLSCRASQSY-----SYLA 54
 Db 1 MEAPQALLFLMLPDTGEIVLTQSPATLSLSPGERATLSCRASQSY-----SYLA 54
 QY 55 WYQKPGQAPRLIYDASNRATGIPRFSGSGGTDFLTLSLPEDEVALYVCOQYFTT 114
 Db 61 WYQKPGQAPRLIYDASNRATGIPRFSGSGGTDFLTLSLPEDEVALYVCOQYFTT 114
 QY 115 PYFGGCTLEIKRTVAASVFIPEPSDEQLKSGTASVYCLLNFFPREAKYQMKVDNAL 174
 Db 121 PLTFGGTVEIKRTVAASVFIPEPSDEQLKSGTASVYCLLNFFPREAKYQMKVDNAL 180
 QY 175 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 8
 US-07-916-098A-56
 Sequence 56, Application US/07916098A
 Patent No. 5871732
 GENERAL INFORMATION:
 APPLICANT: BURKLEY, LINDA C.
 APPLICANT: CHISOLM, PATRICIA L.
 APPLICANT: THOMAS, DAVID W.
 APPLICANT: ROSA, MARGARET D.
 TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 NUMBER OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 CORRESPONDENCE ADDRESS:
 ADDRESS: ALLEGRETTI & WITCOFF, LTD.
 STREET: 10 SOUTH WACKER DRIVE
 CITY: CHICAGO
 STATE: ILLINOIS
 COUNTRY: U.S.A.
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916,098A
 FILING DATE: July 24, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08843
 FILING DATE: No. 5871732ember 27, 1991
 APPLICATION NUMBER: 424
 FILING DATE: No. 5871732ember 27, 1990
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: JOHN J. MC DONNELL

```

REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098a-56

Query Match      82.1%; Score 994.5; DB 2; Length 241;
Best Local Similarity 80.8%; Pred. No. 9,9e-74;
Matches 194; Conservative 20; Mismatches 19; Indels 7; Gaps 2;

QY 1 MEAPQILFLILMLPTTGEIVLTOSPATLSLSPGRATLSGRASQSV-----SSYLA 54
DB 3 MRVPAQLGLLMLLPKARGDIVATQSPDSLAVSLGERATINKSSGSLITSTNKNYLA 62
QY 55 WYQKPGQAPRLLYDASNRAIGIPRRSGSGSGTDTLTISRLEPEDVALYICQGYFTT 114
DB 63 WYQKPGQAPRLLYMASTRESGVDRFSGSGSGTDTLTISRLEPEDVALYICQGYFTT 122
QY 115 FYTGQGRLEIKRTVAAPSVFIFFPPSDQLKSGTASVCLLNPFYPREAKVQKVDNL 174
DB 123 RTFRGRGLKIKRTVAAPSVFIFFPPSDQLKSGTASVCLLNPFYPREAKVQKVDNL 181
QY 175 QSGNQSSEVTQDSKDSYSLSTLTLSKADYEKHYACEVTHOGISLSPVTKSPNREGC 234
DB 182 QSGNQSSEVTQDSKDSYSLSTLTLSKADYEKHYACEVTHOGISLSPVTKSPNREGC 241

RESULT 9
US-08-480-753-6
Sequence 6, Application US/08480753
Patent No. 5830675
GENERAL INFORMATION:
APPLICANT: Targan M.D., Stephan R.
APPLICANT: Vidich Ph.D., Alda M.
TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Wendy A. Whiteford, Esq.
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whiteford, Wendy A.
REGISTRATION NUMBER: 36,964
REFERENCE/DOCKET NUMBER: P07 33571
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-753-6

Query Match      80.8%; Score 979.5; DB 2; Length 214;
Best Local Similarity 89.6%; Pred. No. 1.4e-72;
Matches 190; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 24 LTOSPATLSLSPGRATLSGRASQSVS-STYAMVQKPGQAPRLLYDASNRAIGIPRR 82
DB 3 LTOSPATLSLSPGRATLSGRASQSVSTSTYAMVQKPGQAPRLLYDASNRAIGIPRR 62
QY 83 SGSGSGTDTLTISRLEPEDVALYICQGYFTTPTTGQGRLEIKRTVAAPSVFIFFPSD 142
DB 63 SASWSGDTFTLTISRLEPEDFAVYICQHYGSPWTEGQTKYKRTVAAPSVFIFFPSD 122
QY 143 EQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNQSSEVTQDSKDSYSLSTLTLS 202
DB 123 EQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNQSSEVTQDSKDSYSLSTLTLS 182
QY 203 KADYEKHYACEVTHOGISLSPVTKSPNREGC 234
DB 183 KADYEKHYACEVTHOGISLSPVTKSPNREGC 214

RESULT 10
US-09-041-889-11
Sequence 11, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Ofer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PW 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-889-11

Query Match      80.8%; Score 979.5; DB 3; Length 214;
Best Local Similarity 89.6%; Pred. No. 1.4e-72;

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Matches 190; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 24 LTQSPATLSLSPGERATISCRASQSVS-SYLAWYQOKPGQAPRLIYDASNRAATGIPPR 82
 DB 3 LTQSPATLSLSPGERATISCRASQSVS-SYLAWYQOKPGQAPRLIYDASNRAATGIPPR 62
 QY 83 SSGSGTDFLTITSLRLEPEDVALYCCOQYFTTPTFGQTRLEIKRTVAAPSVFIIPPSD 142
 DB 63 SASMSGTDFLTITSLRLEPEDVALYCCOQYFTTPTFGQTRLEIKRTVAAPSVFIIPPSD 122
 QY 143 EQLSGTASVYCLNNFYPREAKQKVDNALQSGNSQESVTEQDSKDSSTLSLTLS 202
 DB 123 EQLSGTASVYCLNNFYPREAKQKVDNALQSGNSQESVTEQDSKDSSTLSLTLS 182
 QY 203 KADYKHKVYACEVTHOGLSSPYTKSPNRGEC 234
 DB 183 KADYKHKVYACEVTHOGLSSPYTKSPNRGEC 214

RESULT 11
 US-08-837-058-11

Sequence 11, Application US/08837058
 Patent No. 6074835

GENERAL INFORMATION:

APPLICANT: Braun, Jonathan
 APPLICANT: Targan, Mark

APPLICANT: Eggena, Mark

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/837,058

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-PM 2438

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-8849

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-837-058-11

Query Match 80.8%; Score 979.5; DB 3; Length 214;
 Best Local Similarity 89.6%; Pred. No. 1.4e-72;

Matches 190; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 24 LTQSPATLSLSPGERATISCRASQSVS-SYLAWYQOKPGQAPRLIYDASNRAATGIPPR 82
 DB 3 LTQSPATLSLSPGERATISCRASQSVS-SYLAWYQOKPGQAPRLIYDASNRAATGIPPR 62
 QY 83 SSGSGTDFLTITSLRLEPEDVALYCCOQYFTTPTFGQTRLEIKRTVAAPSVFIIPPSD 142
 DB 63 SASMSGTDFLTITSLRLEPEDVALYCCOQYFTTPTFGQTRLEIKRTVAAPSVFIIPPSD 122

QY 143 EQLSGTASVYCLNNFYPREAKQKVDNALQSGNSQESVTEQDSKDSSTLSLTLS 202
 DB 123 EQLSGTASVYCLNNFYPREAKQKVDNALQSGNSQESVTEQDSKDSSTLSLTLS 182
 QY 203 KADYKHKVYACEVTHOGLSSPYTKSPNRGEC 234
 DB 183 KADYKHKVYACEVTHOGLSSPYTKSPNRGEC 214

RESULT 12

US-08-487-550-6

Sequence 6, Application US/08487550

Patent No. 611898

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-6620

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-550-6

Query Match 79.9%; Score 968.5; DB 3; Length 239;
 Best Local Similarity 78.2%; Pred. No. 1.3e-71;

Matches 187; Conservative 23; Mismatches 24; Indels 5; Gaps 1;

QY 1 MEAPQLLELLMLPDTGEIVLTQSPATLSLSPGERATISCRASQSV-----SYLAW 55
 DB 1 MEAPQLLELLMLPDTGEIVLTQSPATLSLSPGERATISCRASQSV-----SYLAW 60
 QY 56 YQKPGQAPRLIYDASNRAATGIPPRSGSGGSDTFTLTSLRLEPEDVALYCCOQYFTTP 115
 DB 61 YQKPGQAPRLIYDASNRAATGIPPRSGSGGSDTFTLTSLRLEPEDVALYCCOQYFTTP 120
 QY 116 YTFGGTFLRLEIKRTVAAPSVFIIPPSDEQLKSGTASVYCLNNFYPREAKQKVDNALQ 175
 DB 121 PTFGGTFLRLEIKRTVAAPSVFIIPPSDEQLKSGTASVYCLNNFYPREAKQKVDNALQ 180
 QY 176 SGNQESVTEQDSKDSSTYSLSLTLSKADYKHKVYACEVTHOGLSSPYTKSPNRGEC 234
 DB 181 SGNQESVTEQDSKDSSTYSLSLTLSKADYKHKVYACEVTHOGLSSPYTKSPNRGEC 239

RESULT 13
US-08-480-753-8

Sequence 8, Application US/08480753
Patent No. 5830675

GENERAL INFORMATION:

APPLICANT: Targan M.D., Stephan R.
APPLICANT: Vidlich Ph.D., Alda M.

TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF

TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR

TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wendy A. Whiteford, Esq.
STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,753

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Whiteford, Wendy A.

REGISTRATION NUMBER: 36,964

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-480-753-8

Query Match

Best Local Similarity 89.2%; Score 968; DB 2; Length 215;

Matches 190; Conservative 10; Mismatches 11; Indels 2; Gaps 2;

QY 24 LTQSPATLSLSPGERATLSCRASQSVS-YLAMYQKRPQAPRLIYDASNRATGIPPRF 82

DB 3 LTQSPATLSLSPGERATLSCRASQSVSGLAYQKQAPRLIYDASNRATGIPPRF 62

QY 83 SGSSGSDFTLTLRLPEDEVALYCCQYFTTP-YTFGGQTRLEIKRTVAAPSVFIFPPS 141

DB 63 TGSSGSDFTLTLRLPEDEVALYCCQYFTTP-YTFGGQTRLEIKRTVAAPSVFIFPPS 122

QY 142 DEQKSGTAVVCLLNFPYREKVKQKVDNALQSGNSQSEVTEQDSKSTYSLSSTLT 201

DB 123 DEQKSGTAVVCLLNFPYREKVKQKVDNALQSGNSQSEVTEQDSKSTYSLSSTLT 182

QY 202 SKADYEKKYVACEVTHQGLSSPYTKSPFNQEC 234

DB 183 SKADYEKKYVACEVTHQGLSSPYTKSPFNQEC 215

RESULT 14

US-09-301-593-28

Sequence 28, Application US/09301593A

Patent No. 6455677

GENERAL INFORMATION:

APPLICANT: Park, John E.

APPLICANT: Garlin-Chesa, Pilar

APPLICANT: Bamberger, Uwe

APPLICANT: Leger, Olivier

APPLICANT: Saidanba, Jose W.
APPLICANT: Rettig, Wolfgang J.

TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A

EARLIER FILING DATE: 1999-04-29

EARLIER APPLICATION NUMBER: EP 98107925.4

EARLIER FILING DATE: 1998-04-30

EARLIER APPLICATION NUMBER: US 60/086,049

EARLIER FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 28

LENGTH: 240

TYPE: PR

ORGANISM: Homo sapiens

US-09-301-593-28

Query Match

Best Local Similarity 75.8%; Score 961; DB 4; Length 240;

Matches 182; Conservative 31; Mismatches 21; Indels 6; Gaps 1;

QY 1 MEAPQLEFLILMLPTGIVLTQSPATLSLSPGERATLSCRASQSV-----SSYLA 54

DB 1 MDSQAVMLPLPWSGTCIDIVMSQSSSLAVSGEKVTMSCKSSQSLYSRQKNTLA 60

QY 55 WTQKRGAPRLIYDASNRATGIPPRFSGSGSDFTLTLRLPEDEVALYCCQYFTT 114

DB 61 WTQKRGAPRLIYDASNRATGIPPRFSGSGSDFTLTLRLPEDEVALYCCQYFTT 120

QY 115 PTFGGQTRLEIKRTVAAPSVFIFPPSDEQKSGTAVVCLLNFPYREKVKQKVDNAL 174

DB 121 PTFGGQTRLEIKRTVAAPSVFIFPPSDEQKSGTAVVCLLNFPYREKVKQKVDNAL 180

QY 175 QSGNSQSEVTEQDSKSTYSLSSTLTLSKADYEKKYVACEVTHQGLSSPYTKSPFNQEC 234

DB 181 QSGNSQSEVTEQDSKSTYSLSSTLTLSKADYEKKYVACEVTHQGLSSPYTKSPFNQEC 240

RESULT 15

US-08-157-101A-5

Sequence 5, Application US/08157101A

Patent No. 5808032

GENERAL INFORMATION:

APPLICANT: KURIHARA, TATSUYA

APPLICANT: MATSUKURA, SHIGEKAZU

APPLICANT: TSURUOKA, NOBUO

APPLICANT: ARIMA, KENJI

APPLICANT: NISHIHARA, TATSURO

TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION

TITLE OF INVENTION: PLASMIDS THEREFOR

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY, MADISON & SUTRO

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/157,101A

FILING DATE: 05-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: TITUS, MARILAN K.

REGISTRATION NUMBER: 35843

REFERENCE/DOCKET NUMBER: 9437/204199

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3711
 ; TELEFAX: 202-822-0944
 ; TELEEX: 6714627 CUCH
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 236 amino acids
 ; TYPE: amino acid
 ; STRADEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-157-101A-5

Query Match

Best Local Similarity 79.0%; Score 958; DB 1; Length 236;
 Matches 181; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

```

QY 1 MEAPADLLFLLMLPDTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLIAMYOQKP 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 MRVPAQLLGLLLMFPGARCDIQMTQSPSMAASVGDRTVITCRASQSIGNTLWVFOQKP 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 GOAPRLIYDASNRATGIPPRSGSGGTDFTLTISRLEPEDVALYCCQYFTPTPTFGQ 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 GKVPKRLIYASSLQSGVPSRFSGSGSGTEFTLTISRLEPEDVALYCCQYFTPTPTFGQ 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 GTRLEIKRIVAAPSVFIIPPSDQELKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQ 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 GTKVEIKRIVAAPSVFIIPPSDQELKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQ 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 ESYTEDSKDSYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 ESYTEDSKDSYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 236
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Search completed: April 23, 2003, 11:03:52
 Job time : 14.4672 secs

QY	1	MEAPAQLLFLMLLPPTTGEIVLQSPATLSISGEKATLSCRASQSY-SSYLAWYQA	3
QY	1	MEAPAQLLFLMLLPPTTGEIVLQSPATLSISGEKATLSCRASQSY-SSYLAWYQA	3
Db	1	MEPPAQLLFLMLLPPTTGEIVLQSPGTLISPEKATLSCRASQMSIRSYLAWYQK	60
QY	60	PEQAPRLLIYASNRATGIPPRFGSGSGGTDTLTIRLEPDAVLYYCOQFTTPY-TF	118
QY	60	PEQAPRLLIYASNRATGIPPRFGSGSGGTDTLTIRLEPDAVLYYCOQFTTPY-TF	118
Db	61	PEQAPGELLYGASRAIGIPPRFGSGSGGTDTLTIRLEPDEDFAYVYCOQFGSPMCST	120
QY	119	GGSTRLEIKRTVAASVFIPEPDSDEQLKSGTAAVYVOLLNPFYPREAKYQMYKDALQSGN	178
QY	119	GGSTRLEIKRTVAASVFIPEPDSDEQLKSGTAAVYVOLLNPFYPREAKYQMYKDALQSGN	178
Db	121	GGGTRLEIKRTVAASVFIPEPDSDEQLKSGTAAVYVOLLNPFYPREAKYQMYKDALQSGN	180

Oy 179 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 2

US-09-859-053-38
 ; Sequence 38, Application US/09859053
 ; Patent No. US20020102658A1
 ; GENERAL INFORMATION:

APPLICANT: Tsuji, Takashi
 APPLICANT: Tezuka, Katsunari
 APPLICANT: Hori, No. US20020102658A1uaki
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIN AND
 FILE REFERENCE: 06501-075001
 CURRENT APPLICATION NUMBER: US/09/859, 053
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: JP 2001-99508
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: JP 2000-147116
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 38
 LENGTH: 236
 TYPE: PRT

ORGANISM: Homo sapiens
 US-09-859-053-38

Query Match
 Best Local Similarity 90.6%; Score 1098; DB 10; Length 236;
 Matches 216; Conservative 9; Mismatches 9; Indels 2; Gaps 2;

Oy 1 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 59
 Db 1 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 60
 Oy 60 PGAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 118
 Db 61 PGAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 118
 Oy 119 GGTGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 178
 Db 121 GGTGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 178
 Oy 179 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 3

US-09-799-514-8
 ; Sequence 8, Application US/09799514
 ; Patent No. US20020065220A1
 ; GENERAL INFORMATION:

APPLICANT: Young et al.
 TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant
 CURRENT APPLICATION NUMBER: US/09/799, 514
 PRIOR FILING DATE: 2001-03-07
 PRIOR APPLICATION NUMBER: PCT/US00/23662
 PRIOR FILING DATE: 2000-08-29
 PRIOR APPLICATION NUMBER: 60/153, 248
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 8
 LENGTH: 240
 TYPE: PRT

ORGANISM: Homo sapiens
 US-09-799-514-8

Query Match
 Best Local Similarity 82.4%; Score 999; DB 10; Length 240;
 Matches 191; Conservative 22; Mismatches 21; Indels 6; Gaps 1;

Oy 1 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 59
 Db 1 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 60
 Oy 55 WYQOKPGQAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 114
 Db 61 WYQOKPGQAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 114
 Oy 115 PYFGGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 174
 Db 121 PYFGGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 174
 Oy 175 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4

US-09-859-053-30
 ; Sequence 30, Application US/09859053
 ; Patent No. US20020102658A1
 ; GENERAL INFORMATION:

APPLICANT: Tsuji, Takashi
 APPLICANT: Tezuka, Katsunari
 APPLICANT: Hori, No. US20020102658A1uaki
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIN AND
 FILE REFERENCE: 06501-079001
 CURRENT APPLICATION NUMBER: US/09/859, 053
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: JP 2001-99508
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: JP 2000-147116
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30
 LENGTH: 236
 TYPE: PRT

ORGANISM: Homo sapiens
 US-09-859-053-30

Query Match
 Best Local Similarity 82.0%; Score 994; DB 10; Length 236;
 Matches 190; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

Oy 1 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 59
 Db 3 MEAPQALLFLLLMLPDTTGEIYVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOK 60
 Oy 61 PGAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 118
 Db 63 PGAPRLIYDASNRATGIPPRFSGSGGDTFTLTISLSEPEDEVALYCCOQYFTTPY-TF 118
 Oy 121 GGTGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 174
 Db 123 GGTGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVDNALQSGN 174
 Oy 181 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 183 SOESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 5

US-09-249-011A-22
 ; Sequence 22, Application US/09249011A
 ; Patent No. US20020176855A1

QY 176 SGNSESVTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 SGNSESVTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
 US-09-740-002-24

Sequence 24, Application US/09740002
 Patent No. US20020001798A1
 GENERAL INFORMATION:

APPLICANT: BRAMS, PETER
 APPLICANT: MORROW, PHILLIP
 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
 FILE REFERENCE: 037003-0275759
 CURRENT APPLICATION NUMBER: US/09/740,002
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 09/335,697
 PRIOR FILING DATE: 1999-06-18
 PRIOR APPLICATION NUMBER: 08/488,376
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 24
 LENGTH: 234
 TYPE: PRF
 ORGANISM: Homo sapiens

US-09-740-002-24

Query Match
 Best Local Similarity 80.3%, Score 989; DB 10; Length 234;
 Matches 188; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 1 MEAPQQLFLLLMPTTGIVLTOSPATLSLSPGERATLSGRASQSVSYLAWYQKP 60
 Db 1 MEAPQQLFLLLMPTTGIVLTOSPATLSLSPGERATLSGRASQSVSYLAWYQKP 60
 QY 61 GKAPLLIYDASNRATGIPRPSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGQ 120
 Db 61 GKAPLLIYDASNRATGIPRPSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGQ 120
 QY 121 GTREIKRTVAAPSVTFPPPSDQLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQ 180
 Db 121 GTREIKRTVAAPSVTFPPPSDQLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQ 180
 QY 181 ESYTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 ESYTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 9
 US-10-006-593-118

Sequence 118, Application US/10006593
 Publication No. US20030049683A1
 GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

FILE REFERENCE: 1087-2
 CURRENT APPLICATION NUMBER: US/10/006,593
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: 06/251,448
 PRIOR FILING DATE: 2000-12-05
 PRIOR APPLICATION NUMBER: US 60/288,889
 PRIOR FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: US 60/294,068
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentln version 3.1
 SEQ ID NO 118

LENGTH: 212
 TYPE: PRF
 ORGANISM: human
 US-10-006-593-118

Query Match
 Best Local Similarity 91.0%, Score 986; DB 9; Length 212;
 Matches 193; Conservative 8; Mismatches 9; Indels 2; Gaps 2;

QY 24 LTOSPATLSLSPGERATLSGRASQSVSYLAWYQKQAPRLLIYDASNRATGIPRPF 82
 Db 2 LTOSPATLSLSPGERATLSGRASQSVSYLAWYQKQAPRLLIYDASNRATGIPRPF 82
 QY 83 SSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGTLEIKRTVAAPSVTFPPSD 142
 Db 62 SSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGTLEIKRTVAAPSVTFPPSD 142
 QY 143 EOLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQSVTEQDSKSTYSLSSTLTLS 202
 Db 121 EOLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQSVTEQDSKSTYSLSSTLTLS 202
 QY 203 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 181 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 10
 US-10-006-593-69

Sequence 69, Application US/10006593
 Publication No. US20030049683A1
 GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
 FILE REFERENCE: 1087-2
 CURRENT APPLICATION NUMBER: US/10/006,593
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: US 60/251,448
 PRIOR FILING DATE: 2000-12-05
 PRIOR APPLICATION NUMBER: US 60/288,889
 PRIOR FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: US 60/294,068
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentln version 3.1
 SEQ ID NO 69
 LENGTH: 236
 TYPE: PRF
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: Humanized antibody light chain

US-10-006-593-69

Query Match
 Best Local Similarity 80.8%, Score 979; DB 9; Length 236;
 Matches 188; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEAPQQLFLLLMPTTGIVLTOSPATLSLSPGERATLSGRASQSVSYLAWYQKP 60
 Db 3 MEAPQQLFLLLMPTTGIVLTOSPATLSLSPGERATLSGRASQSVSYLAWYQKP 60
 QY 61 GKAPLLIYDASNRATGIPRPSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGQ 120
 Db 63 GKAPLLIYDASNRATGIPRPSGSGGDTFTLTISRLEPEDVALYCCOQYTFPTTGGQ 120
 QY 121 GTREIKRTVAAPSVTFPPPSDQLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQ 180
 Db 123 GTREIKRTVAAPSVTFPPPSDQLKSGTASVYCLNNFYPREAVQKVDNALQSGNSQ 180
 QY 181 ESYTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
 Db 183 ESYTEQDSKSTYSLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 236

Wed Apr 23 13:51:08 2003

us-09-806-276a-1.rapb

RESULT 11
US-10-124-905-6 Application US/10124905
Sequence 6, Application US/10124905

GENERAL INFORMATION: Darrell R. Anderson, "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/124,905

CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-10-124-905-6 79.9%; Score 968.5; DB 9; Length 239; Indels 5; Gaps 1;
Query Match 78.2%; Pred. No. 1.3e-38; Mismatches 24;

Best Local Similarity 78.2%; Conservative 23; Mismatches 24; Indels 5; Gaps 1;
Matches 187; Conservative 23; Mismatches 24; Indels 5; Gaps 1;
QY 1 MEAPQLFLILMLPDTGRIYVLOSPLSLSPGERATLSGRASQV-----SSYLAW 55
DB 1 MSIPQLGLLILCVPSGSEVMTOSPLSLPTEPEPASISCRSSOSLSKNSGDTFLSW 60
QY 56 YQKFGQAPRLIYDASNRATGIPRFGSGSGDTFTLTSRLPEEDVALYCOQYFTTP 115
DB 121 PTFGGTVEIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
QY 116 YTGQGTREIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 175
DB 61 YQKFGQAPRLIYDASNRATGIPRFGSGSGDTFTLTSRLPEEDVALYCOQYFTTP 120
QY 116 YTGQGTREIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
DB 121 PTFGGTVEIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
QY 176 SGNQSEVTEODSKDSTYSLSSTLTLSKADYEKHKYACVETHQGLSSPYTSFNRGEC 234
DB 181 SGNQSEVTEODSKDSTYSLSSTLTLSKADYEKHKYACVETHQGLSSPYTSFNRGEC 239

RESULT 12
US-09-948-429B-6 Application US/09948429B
Sequence 6, Application US/09948429B

Patent No. US20020177689A1

GENERAL INFORMATION: Darrell R. Anderson, "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/948,429B

CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-948-429B-6 79.9%; Score 968.5; DB 9; Length 239; Indels 5; Gaps 1;
Query Match 78.2%; Pred. No. 1.3e-38; Mismatches 24;

Best Local Similarity 78.2%; Conservative 23; Mismatches 24; Indels 5; Gaps 1;
Matches 187; Conservative 23; Mismatches 24; Indels 5; Gaps 1;
QY 1 MEAPQLFLILMLPDTGRIYVLOSPLSLSPGERATLSGRASQV-----SSYLAW 55
DB 1 MSIPQLGLLILCVPSGSEVMTOSPLSLPTEPEPASISCRSSOSLSKNSGDTFLSW 60
QY 56 YQKFGQAPRLIYDASNRATGIPRFGSGSGDTFTLTSRLPEEDVALYCOQYFTTP 115
DB 121 PTFGGTVEIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
QY 116 YTGQGTREIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 175
DB 61 YQKFGQAPRLIYDASNRATGIPRFGSGSGDTFTLTSRLPEEDVALYCOQYFTTP 120
QY 116 YTGQGTREIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
DB 121 PTFGGTVEIKRTVAAPSVFIPEPSDEOLKSGTASVCLNNFYPREAKYQMKVDNALQ 180
QY 176 SGNQSEVTEODSKDSTYSLSSTLTLSKADYEKHKYACVETHQGLSSPYTSFNRGEC 234
DB 181 SGNQSEVTEODSKDSTYSLSSTLTLSKADYEKHKYACVETHQGLSSPYTSFNRGEC 239

RESULT 13
US-09-740-002-26 Application US/09740002
Sequence 26, Application US/09740002
Patent No. US20020001798A1
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
 FILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
 CURRENT REFERENCE: 037003-0275759
 CURRENT APPLICATION NUMBER: US/09/740,002
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 09/735,697
 PRIOR FILING DATE: 1999-06-18
 PRIOR APPLICATION NUMBER: 08/488,376
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 26
 LENGTH: 234
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-740-002-26

Query Match
 Best Local Similarity 79.5%; Score 963.5; DB 10; Length 234;
 Matches 187; Conservative 24; Mismatches 23; Indels 1; Gaps 1;

QY 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAQSVSYLAWYQKP 60
 DB 3 MRVPAQLLGLLLMLNGARCDIOMTOSPSLSASVGDRTVITCRASQSIASVYMWYQKP 60
 QY 61 GOAPRLIYDASNRTGIPRFGSGSGGDTFTLTSLRLEPEDVALYCCOQYFTPTTQ 62
 DB 63 GKAPVLLFASANLVSGVPSRFGSGSGGVFTLTSLNLPEDFAFYCCOQYFTPTTQ 62
 QY 121 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 DB 122 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 QY 181 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 233
 DB 182 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 14
 US-09-800-729-150

Sequence 150, Application US/09800729
 Patent No. US20020068319A1
 GENERAL INFORMATION:
 APPLICANT: NI et al.
 TITLE OF INVENTION: 32 Human secreted proteins
 FILE REFERENCE: P2044P1
 CURRENT APPLICATION NUMBER: US/09/800,729
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: PCT/US00/26013
 PRIOR FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 60/155,709
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 150
 LENGTH: 234
 TYPE: PRT
 ORGANISM: Homo sapiens
 NAME/KEY: SITE
 LOCATION: (120)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-09-800-729-150

Query Match
 Best Local Similarity 78.9%; Score 956; DB 10; Length 234;
 Matches 187; Conservative 20; Mismatches 31; Indels 0; Gaps 0;
 QY 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAQSVSYLAWYQKP 60
 DB 1 MRVPAQLLGLLLMLNGARCDIOMTOSPSLSASVGDRTVITCRASQSIASVYMWYQKP 60
 QY 61 GOAPRLIYDASNRTGIPRFGSGSGGDTFTLTSLRLEPEDVALYCCOQYFTPTTQ 60

DB 61 GKAPVLLFASANLVSGVPSRFGSGSGGVFTLTSLNLPEDFAFYCCOQYFTPTTQ 62
 QY 121 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 DB 122 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 QY 181 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 233
 DB 182 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 15
 US-09-800-729-152

Sequence 152, Application US/09800729
 Patent No. US20020068319A1
 GENERAL INFORMATION:
 APPLICANT: NI et al.
 TITLE OF INVENTION: 32 Human secreted proteins
 FILE REFERENCE: P2044P1
 CURRENT APPLICATION NUMBER: US/09/800,729
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: PCT/US00/26013
 PRIOR FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 60/155,709
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 152
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-800-729-152

Query Match
 Best Local Similarity 78.8%; Score 955.5; DB 10; Length 235;
 Matches 187; Conservative 16; Mismatches 30; Indels 1; Gaps 1;

QY 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAQSVSYLAWYQKP 60
 DB 3 MRVPAQLLGLLLMLNGARCDIOMTOSPSLSASVGDRTVITCRASQSIASVYMWYQKP 60
 QY 61 GOAPRLIYDASNRTGIPRFGSGSGGDTFTLTSLRLEPEDVALYCCOQYFTPTTQ 62
 DB 63 GKAPVLLFASANLVSGVPSRFGSGSGGVFTLTSLNLPEDFAFYCCOQYFTPTTQ 62
 QY 121 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 DB 122 GTRLEIKRTVAAPSVFTFPSPDEQLKSGTASVYCLNNFYPREAKYQKVDNALQSGNSQ 120
 QY 181 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 233
 DB 182 ESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHOGLSSPVTKSFNRGEC 234

Search completed: April 23, 2003, 11:04:28
 Job time: 15.3852 secs

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OM protein - protein search, using sw model

Run on: April 23, 2003, 10:58:30 ; Search time 13.9057 Seconds
(without alignments)
1617.710 Million cell updates/sec

Title: US-09-806-276A-1
Perfect score: 1212
Sequence: 1 MEAPAGLLFLLLMLPDTG.....EYHOGLSPPVTKSFNRGEC 234

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR-73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1018.5	84.0	215	2 JE0242	Ig kappa chain NIG
2	993.5	82.0	215	2 JE0244	Ig kappa chain NIG
3	974.5	80.4	215	2 A23746	Ig kappa chain V-I
4	956.5	78.9	216	2 JE0243	Ig kappa chain NIG
5	899	74.2	216	2 JE0241	Ig kappa chain Am3
6	806	66.5	240	2 S06084	Ig kappa chain pre
7	741	61.1	234	2 S01320	Ig kappa chain pre
8	740	61.1	234	2 S14237	Ig kappa chain pre
9	736.5	60.8	230	2 S33161	Ig kappa chain - s
10	726.5	59.9	225	2 S37484	Ig kappa chain - m
11	717	59.2	218	2 S68241	Ig kappa chain V r
12	712.5	58.8	219	2 S38865	Ig kappa chain - m
13	712	58.7	220	2 A31790	Ig kappa chain V r
14	711	58.7	218	2 JC5810	Ig kappa chain V r
15	706	58.3	214	2 S68212	Ig kappa chain (Ma
16	703.5	58.0	219	2 S52028	Ig kappa chain - m
17	703.5	58.0	235	2 S25058	Ig kappa chain - m
18	700.5	57.8	219	2 PC4203	Ig kappa chain (mo
19	700.5	57.8	219	2 S16112	Ig kappa chain V r
20	698.5	57.6	217	2 S42772	Ig kappa chain - m
21	693	57.2	210	2 A56169	Ig kappa chain V r
22	680.5	56.1	225	2 JL0029	Ig kappa chain pre
23	671	55.4	244	2 PL0106	Ig kappa chain pre
24	613.5	50.6	145	2 S20631	Ig kappa chain - h
25	613	50.6	178	2 PT0219	Ig kappa chain V-C
26	603.5	49.8	197	2 S29593	Ig kappa chain (WM
27	602	49.7	135	2 S52059	Ig kappa chain pre
28	589.5	48.6	129	1 K3H04	Ig kappa chain pre
29	589.5	48.6	229	2 A20969	Ig kappa chain pre

30	584.5	48.2	129	2 S49532	anti-sm antibody V
31	583.5	48.1	129	1 K3H04	Ig kappa chain pre
32	581.5	48.0	129	2 S46369	Ig light chain var
33	581.5	48.0	134	2 S38643	Ig kappa chain V r
34	580	47.9	128	2 S40379	Ig kappa chain V-J
35	577.5	47.6	128	2 S20636	Ig kappa chain V r
36	576	47.5	128	2 A56701	Ig kappa chain V r
37	573	47.3	128	1 K3H04	Ig kappa chain pre
38	572.5	47.2	129	2 S40363	Ig kappa chain - h
39	572.5	47.2	238	2 A49633	Ig lambda-like cha
40	571.5	47.2	128	2 A32274	Ig kappa chain pre
41	567	46.8	128	2 S40343	Ig kappa chain V-J
42	565	46.1	125	2 S40344	Ig kappa chain V-J
43	558	46.0	139	2 S29627	Ig kappa chain V r
44	557.5	46.0	130	2 S20637	Ig kappa chain V r
45	555.5	45.8	121	2 S40327	Ig kappa chain - h

ALIGNMENTS

RESULT 1

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <Alt>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 84.0% Score 1018.5; DB 2; Length 215;

Best Local Similarity 92.6% Pred. No. 3.3e-62; Mismatches 9; Indels 1; Gaps 1;

Matches 199; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY	21	EYLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQKPGAPRLIYDASNRARGIP	79
DB	1	EYLTQSPATLSLSPGERATLSCRASQSVSNNYLAWYQKPGAPRLIYDASNRARGIP	60
QY	80	PRESGSGSTFTLTISRLPEPDVALTYCOOFTTPYRFGGTLEKRYVAASVFIFP	139
DB	61	DRFSGSGSTFTLTISRLPEPDVALTYCOOFTTPYRFGGTLEKRYVAASVFIFP	120
QY	140	PSDEIKSGTASVYCLNFFPREAKVQKYNALQSNQSESYTEODSKDSTYSLSTL	199
DB	121	PSDEIKSGTASVYCLNFFPREAKVQKYNALQSNQSESYTEODSKDSTYSLSTL	180
QY	200	TLSKADYEKKHYKACEVTHQGLSSPVTKSFNRGEC	234
DB	181	TLSKADYEKKHYKACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.

submitted to JIPID, November 1998

A:Description: A new subgroup of kappa type light chains (YKV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 993.5; DB 2; Length 215;
 Best Local Similarity 91.2%; Pred. No. 1.6e-60;
 Matches 196; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIPP 80
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIPA 60
 QY 81 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 139
 DB 61 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 120
 QY 140 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 199
 DB 121 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 180
 QY 200 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 234
 DB 181 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 215

RESULT 3

A23746

Ig kappa chain V-III (KAV cold agglutinin) - human

C:Species: Homo sapiens (man)

C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C:Accession: A23746

R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immunoglobulin

A:Reference number: A23746; MIMD:9131575; PMID:1993660

A:Accession: A23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-215 <LEO>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 974.5; DB 2; Length 215;
 Best Local Similarity 92.1%; Pred. No. 3.2e-59;
 Matches 197; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIPP 79
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIP 60
 QY 80 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 139
 DB 61 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 120
 QY 140 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 199
 DB 121 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 180
 QY 200 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 233
 DB 181 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 214

RESULT 4

JEO243

Ig kappa chain NIC93 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JEO243

R:Allm, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazl, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JEO243

A:Accession: JEO243

A:Molecule type: protein

A:Residues: 1-215 <ALT>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.9%; Score 956.5; DB 2; Length 215;
 Best Local Similarity 87.0%; Pred. No. 5.2e-58;
 Matches 187; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIPP 80
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRATGIPA 60
 QY 81 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 139
 DB 61 RFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 120
 QY 140 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 199
 DB 121 PSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 180
 QY 200 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 234
 DB 181 TLSKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 215

RESULT 5

JEO241

Ig kappa chain Am37 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JEO241

R:Allm, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JEO241

A:Molecule type: protein

A:Residues: 1-216 <ALT>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 899; DB 2; Length 216;
 Best Local Similarity 81.2%; Pred. No. 4.1e-54;
 Matches 177; Conservative 19; Mismatches 16; Indels 6; Gaps 3;

QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRAT 76
 DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLITYDASNRAT 76
 QY 77 GIPRFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 136
 DB 59 GIPRFGSGSGDTFTLTISRLEPEDVALYCCOQYFTPTPTFGGTRLEIKRTVAAPSVFIIP 118
 QY 137 IFPPDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 196
 DB 119 IFPPDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQESYTEDDSKDSYSLSTL 178
 QY 197 STLTSLKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 234
 DB 179 STLTSLKADYEKKHYVACEVTHQGLSSPYTKSFNRGEC 216

RESULT 6

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3, rat myeloma immunoglobulin kappa chain c

A:Reference number: S06084; MIMD:90016888; PMID:2508067

A:Accession: S06084

Query 185 EODSKSTYSLSTLTKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234
 Db 181 DODSKSTYSLSTLTKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234
 S37484
 RESULT 10
 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
 R:Accession: S37484
 Submitted to the EMBL Data Library, February 1993
 A:Accession number: S37483
 A:Status: preliminary
 A:Residues: 1-225 <DUC>
 A:Cross-references: EMBL:X70424; NID:9406254; PID:CAA49869.1; PID:9406255
 C:Keywords: heterotetramer; immunoglobulin

Query Match
 Best Local Similarity 59.9%; Score 726.5; DB 2; Length 225;
 Matches 137; Conservative 38; Mismatches 48; Indels 1; Gaps 1;
 QY 11 LLLMLDPTGETVLTQSPATLSLSPGERATLSCRASSQSYSLAWYQOKRGPRLITYD 70
 Db 3 LLLCSGAGSIVMTQPRKFLISAGDRTVTCRASSVNDVAMVQOKRGPRLITYD 70
 QY 71 ASNRATGTPRFGSGSGSDPTLTLSRLPEEDVALYCCQYFTTPYFGGTRLEIKRTVAAPSV 136
 Db 63 ASSRTGVDPKFGSGYGTDFEFTSTVQAEADLVYFCQODSS-YFGGGTRLEIKRTVAAPSV 136
 QY 131 AASVVFPPSDQKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 121
 Db 122 AARTVVFPPSDQKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 121
 QY 191 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234
 Db 182 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234

RESULT 11
 S68241
 Ig kappa chain V region (Mab13-1) - mouse (fragment)
 N:Alternate names: Immunoglobulin light chain
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 R:Accession: S68241; S68214
 Submitted to the EMBL Data Library, March 1994
 A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
 A:Accession number: S68241
 A:Residues: 1-218 <TRK>
 A:Cross-references: EMBL:D29670; NID:9473962; PID:AAA06141.1; PID:9473963
 R:Title: Thermolabile peroxidase activity with a recombinant antibody L chain-porphyrin
 A:Reference number: S68211; MUID:96085223; PMID:7498516
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-218 <TRK>
 A:Cross-references: EMBL:D29670
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match
 Best Local Similarity 62.8%; Score 717; DB 2; Length 218;
 Matches 137; Conservative 31; Mismatches 46; Indels 4; Gaps 1;

Query 21 EIVLTQSPATLSLSPGERATLSCRASSQSYSLAWYQOKRGPRLITYDASNRAT 76
 Db 1 ELVLTQSPATLSLSPGERATLSCRASSQSYSLAWYQOKRGPRLITYDASNRAT 76
 QY 77 GIPRFGSGSGSDPTLTLSRLPEEDVALYCCQYFTTPYFGGTRLEIKRTVAAPSV 136
 Db 61 GIPRFGSGSGSDPTLTLSRLPEEDVALYCCQYFTTPYFGGTRLEIKRTVAAPSV 136
 QY 137 IFFPSDEQLKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 121
 Db 121 IFFPSDEQLKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 121
 QY 197 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234
 Db 181 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234

RESULT 12
 S38865
 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
 R:Kipp, B.; Becker, W.; Schlaak, M.
 Submitted to the EMBL Data Library, November 1993
 A:Description: Combination of a defined specificity and desired isotype by cloning of
 A:Accession number: S38865
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-219 <KIP>
 A:Cross-references: EMBL:Z27396; NID:9416538; PID:CAA81787.1; PID:9416539
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match
 Best Local Similarity 60.7%; Score 712.5; DB 2; Length 219;
 Matches 133; Conservative 37; Mismatches 44; Indels 5; Gaps 1;
 QY 21 EIVLTQSPATLSLSPGERATLSCRASSQSYSLAWYQOKRGPRLITYDASNRAT 76
 Db 1 ELVLTQSPATLSLSPGERATLSCRASSQSYSLAWYQOKRGPRLITYDASNRAT 76
 QY 76 GIPRFGSGSGSDPTLTLSRLPEEDVALYCCQYFTTPYFGGTRLEIKRTVAAPSV 135
 Db 61 GIPRFGSGSGSDPTLTLSRLPEEDVALYCCQYFTTPYFGGTRLEIKRTVAAPSV 135
 QY 136 IFFPSDEQLKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 120
 Db 121 IFFPSDEQLKSGTASVYCLNFFPRKAVQKVDNALQSGNSQESVTEYDSKD 120
 QY 196 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234
 Db 181 STYLSLTLSKADYEHKRYACEVTHOGLSSPYTKSFNRGEC 234

RESULT 13
 A31790
 Ig kappa chain V region (17/9) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
 R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
 A:Reference number: A92666; MUID:89034213; PMID:3182835
 A:Status: preliminary crystallographic data, primary sequence, and binding data for an
 A:Molecule type: mRNA
 A:Residues: 1-220 <SCH>
 A:Cross-references: GB:M23626; GB:J04061; NID:9533234; PID:AAA9162.1; PID:9533235
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: Immunoglobulin homology <1MM>

Query Match 58.7%; Score 712; DB 2; Length 220;

Best Local Similarity 59.1%; Pred. No. 1.9e-41; Mismatches 44; Indels 6; Gaps 1;

Matches 130; Conservative 40; Mismatches 44; Indels 6; Gaps 1;

QY 21 EYLTQSPATLSLSPGERATLSCRAQSY-----SSYLAWYQKPGQAPRLIYDASNR 74
 DB 1 DYMTOSSPSLVTAGAEKVTMSTCTSSQSLFNSGKQKNYLTWYQKPGQAPRLIYMASTR 60
 QY 75 ATGIPRFGSGSGGTDFTLTISRLPEDEVALYCCQYFTPTFGQGRLEIKRTVAAPS 134
 DB 61 ESGVPDFRTSGSGGTDFTLTISVQAEDLADYFCQOHSTPTFGGRTLEIKRADAPT 120
 QY 135 VFIPPSDEQLKSGTASVCLNNFYPRKAYQKVDNALQSGNSQESVTEODSKDSTYS 194
 DB 121 VSIFPPSEQLITSGASVCFELNNFYPKDINVKWKIDGSEKQNGVLSWTDQSDKSTYS 180
 QY 195 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKS 234
 DB 181 MSTLTITLKDEYERHNSYTCEATHKSTSPVKSFNRMNC 220

RESULT 14

JC5810 monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JC5810

R:Kashih, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A:Reference number: JC5810; MUID:98063277; PMID:9398605

A:Accession: JC5810

A:Molecule type: protein

A:Residues: 1-218 <AKR>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin

C:Superfamily: Immunoglobulin V region: Immunoglobulin homology

F:16-94/Domain: Immunoglobulin homology <1MM>

Query Match 58.7%; Score 711; DB 2; Length 218;

Best Local Similarity 63.1%; Pred. No. 2.2e-41; Mismatches 47; Indels 4; Gaps 1;

QY 22 IYLTQSPATLSLSPGERATLSCRAQSY-----YLAHYQKPGQAPRLIYDASNRATG 77
 DB 2 IYLTQSPATLSLSPGERATLSCRAQSY-----YLAHYQKPGQAPRLIYDASNRATG 61
 QY 78 IPRFSGSGSGGTDFTLTISRLPEDEVALYCCQYFTPTFGQGRLEIKRTVAAPSVEI 137
 DB 62 VPARFSGSGSGGTDFTLTINHPVEEDVATYCCQHSRELPLTFGAGTKLELRADAPVSI 121
 QY 138 FPPSDQLKSGTASVCLNNFYPRKAYQKVDNALQSGNSQESVTEODSKDSTYSLS 197
 DB 122 FPPSSQLITSGASVCFELNNFYPKDINVKWKIDGSEKQNGVLSWTDQSDKSTYSMS 181
 QY 198 TLTLSKADYEKKHYACEVTHQGLSPVTKS 234
 DB 182 TLTLTLDKDEYERHNSYTCEATHKSTSPVKSFNRMNC 218

RESULT 15

S68212

Ig kappa chain (Mab03-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000

C:Accession: S68212

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A:Reference number: S68211; MUID:96085223; PMID:7498516

A:Accession: S68212

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-214 <TAK>

A:Cross-references: EMBL:D29668

C:Superfamily: Immunoglobulin V region: Immunoglobulin homology

Query Match 58.3%; Score 706; DB 2; Length 214;

Best Local Similarity 60.3%; Pred. No. 4.7e-41; Mismatches 38; Indels 6; Gaps 1;

Matches 129; Conservative 41; Mismatches 38; Indels 6; Gaps 1;

QY 21 EYLTQSPATLSLSPGERATLSCRAQSY-----SSYLAWYQKPGQAPRLIYDASNR 74
 DB 1 DYMTOSSPSLAVQKVTMSTCTSSQSLFNSGKQKNYLTWYQKPGQAPRLIYFASTR 60
 QY 75 ATGIPRFGSGSGGTDFTLTISRLPEDEVALYCCQYFTPTFGQGRLEIKRTVAAPS 134
 DB 61 ESGVPDFRTSGSGGTDFTLTISVQAEDLADYFCQOHSTPTFGGRTLEIKRADAPT 120
 QY 135 VFIPPSDEQLKSGTASVCLNNFYPRKAYQKVDNALQSGNSQESVTEODSKDSTYS 194
 DB 121 VSIFPPSEQLITSGASVCFELNNFYPKDINVKWKIDGSEKQNGVLSWTDQSDKSTYS 180
 QY 195 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKS 228
 DB 181 MSTLTITLKDEYERHNSYTCEATHKSTSPVKS 214

Search completed: April 23, 2003, 11:03:18
 Job time : 14.9057 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 10:54:35 ; Search time 13.9057 Seconds
(without alignments)
697.946 Million cell updates/sec

Title: US-09-806-276a-1

Perfect score: 1212
Sequence: 1 MEAPPAQLLELLMLPDTTG.....EYTHGGLSSPYTKSFNRGEC 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	589.5	48.6	129 1 KV3L_HUMAN	P18135 homo sapien
2	583.5	48.1	129 1 KV3M_HUMAN	P18136 homo sapien
3	573	47.3	128 1 KV3K_HUMAN	P06311 homo sapien
4	559.5	46.2	129 1 KV3H_HUMAN	P04207 homo sapien
5	548	45.2	106 1 KAC_HUMAN	P01834 homo sapien
6	545	45.0	115 1 KV3I_HUMAN	P04433 homo sapien
7	490.5	40.5	116 1 KV3J_HUMAN	P04434 homo sapien
8	479.5	39.6	109 1 KV3B_HUMAN	P01620 homo sapien
9	477.5	39.4	109 1 KV3D_HUMAN	P01622 homo sapien
10	470.5	38.8	109 1 KV3A_HUMAN	P01623 homo sapien
11	456.5	37.7	108 1 KV3E_HUMAN	P01619 homo sapien
12	453.5	37.4	109 1 KV3G_HUMAN	P04206 homo sapien
13	444	36.6	129 1 KV1W_HUMAN	P04431 homo sapien
14	442	36.5	134 1 KV4C_HUMAN	P06314 homo sapien
15	439.5	36.3	109 1 KV3F_HUMAN	P01624 homo sapien
16	427	35.2	131 1 KV3I_MOUSE	P01661 mus musculu
17	424.5	35.0	100 1 KV3C_HUMAN	P01621 homo sapien
18	423	34.9	132 1 KV3F_MOUSE	P01658 mus musculu
19	422.5	34.8	133 1 KV4B_HUMAN	P06313 homo sapien
20	422	34.8	114 1 KV4A_HUMAN	P01625 homo sapien
21	419	34.6	117 1 KV1J_HUMAN	P01602 homo sapien
22	416.5	34.4	133 1 KV2F_HUMAN	P06310 homo sapien
23	410	33.8	108 1 KV1H_HUMAN	P01600 homo sapien
24	401	33.1	149 1 KV5A_MOUSE	P01603 mus musculu
25	400	33.0	108 1 KV1M_HUMAN	P01605 homo sapien
26	399	32.9	128 1 KV5E_MOUSE	P04432 mus musculu
27	399	32.9	129 1 KV1X_HUMAN	P01594 homo sapien
28	397	32.8	108 1 KV1B_HUMAN	P04430 homo sapien
29	396	32.7	108 1 KV1V_HUMAN	P01593 homo sapien
30	395	32.6	108 1 KV1A_HUMAN	P01590 homo sapien
31	393	32.4	108 1 KV4O_HUMAN	P06312 homo sapien
32	393	32.4	121 1 KV5B_MOUSE	P01634 mus musculu
33	392	32.3	136 1	

34	389	32.1	108 1 KV1L_HUMAN	P01604 homo sapien
35	388	32.0	108 1 KV1E_HUMAN	P01597 homo sapien
36	388	32.0	108 1 KV1K_HUMAN	P01603 homo sapien
37	388	32.0	108 1 KV1N_HUMAN	P01606 homo sapien
38	388	32.0	108 1 KV1Y_HUMAN	P01602 homo sapien
39	385	31.8	108 1 KV1C_HUMAN	P01595 homo sapien
40	383	31.6	111 1 KV3H_MOUSE	P01609 mus musculu
41	382.5	31.6	117 1 KV2E_HUMAN	P06309 homo sapien
42	381.5	31.5	107 1 KV1D_HUMAN	P01596 homo sapien
43	381.5	31.5	113 1 KV2D_HUMAN	P01617 homo sapien
44	381	31.4	108 1 KV1O_HUMAN	P01609 homo sapien
45	381	31.4	111 1 KV3M_MOUSE	P01665 mus musculu

ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD	PRT	Length
AC	P18135	MEAPPAQLLELLMLPDTTG			129 AA
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-II region HAH precursor				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88171307; PubMed=3127527;				
RA	Klips T.J., Tomhave E., Chen P.P., Carson D.A.;				
RT	"Antibody-associated kappa light chain variable region gene				
RT	expressed in chronic lymphocytic leukemia with little or no somatic				
RT	mutation. Implications for etiology and immunotherapy."				
RU	J. Exp. Med. 167:840-852(1988).				
CC	-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M				
CC	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC				
CC	LEUKEMIA.				
DR	PIR; P10022; K3H0HA.				
DR	HSSP; P80362; 1WTL.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; 1g_1.				
DR	SMART; SM00406; 1g_1.				
KW	Immunoglobulin V region; Signal.				
FT	CHAIN	1	20		
FT	DOMAIN	21	129		
FT	DOMAIN	21	43		
FT	DOMAIN	44	55		
FT	DOMAIN	56	70		
FT	DOMAIN	71	77		
FT	DOMAIN	78	109		
FT	DOMAIN	110	118		
FT	DOMAIN	119	129		
FT	DISULFID	43	109		
FT	NON_TER	129	129		
SQ	SEQUENCE	129 AA; 14073 MW; D3C55292772774D0 CRC64;			
QY	Query Match	48.6%; Score 589.5; DB 1; Length 129;			
QY	Best Local Similarity	89.9%; Pred. No. 2.9e-43;			
QY	Matches 116; Conservative	5; Mismatches 7; Indels 1; Gaps 1;			
DB	1 MEAPPAQLLELLMLPDTTG	IVTOSPARLISPGERATLSCASQSVSSVLAWQOK 59			
QY	1 MEAPPAQLLELLMLPDTTG	IVTOSPARLISPGERATLSCASQSVSSVLAWQOK 60			
DB	60 PGAPPRLLIYDASNRATGIPRFGSGSGDTFTLISRLPEVATLYCCOYFTPTFG 119				
QY	61 PGAPPRLLIYDASNRATGIPRFGSGSGDTFTLISRLPEVATLYCCOYFTPTFG 120				
DB	120 OGTRLEIKR 128				

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Db      121 GGTKEIKR 129

|||||
RESULT 2
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig kappa chain V-II region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RA Klapa T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -1 DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR HSP; P10021; K3HUI.
DR HSP; P80362; 1WU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 129
FT DOMAIN 21 129 IG KAPPA CHAIN V-II REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 129 BY SIMILARITY.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match
Best Local Similarity 48.1%; Score 583.5; DB 1; Length 129;
Matches 114; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Db      1 MEAPQLFLLLMLPDTGTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAWYQOK 59
|||
Db      1 METPAQLFLLLMLPDTGTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAWYQOK 60
QY 60 PQQARLLIYDASNRATGIPPRFSGSGGTDTFTLTISRLEPEDVALYCCQYFTPTFG 119
|||
Db      61 PQQARLLIYDASNRATGIPPRFSGSGGTDTFTLTISRLEPEDVALYCCQYFTPTFG 120
|||
QY 120 GGTLEIKR 128
|||
Db      121 GGTKEIKR 129

RESULT 3
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig kappa chain V-II region IARC/BL41 precursor.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL: Z00021; CAA77316.1;
DR HSP; P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 128
FT DOMAIN 21 128 IG KAPPA CHAIN V-II REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JKI SEGMENT.
FT DISULFID 43 128 BY SIMILARITY.
FT NON_TER 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match
Best Local Similarity 47.3%; Score 573; DB 1; Length 128;
Matches 112; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Db      1 MEAPQLFLLLMLPDTGTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAWYQOK 60
|||
Db      1 METPAQLFLLLMLPDTGTGEIVLQSPATLSLSPGERATLSCASQSVSSYLAWYQOK 60
QY 61 GQAPRLIYDASNRATGIPPRFSGSGGTDTFTLTISRLEPEDVALYCCQYFTPTFG 120
|||
Db      61 GQAPRLIYDASNRATGIPPRFSGSGGTDTFTLTISRLEPEDVALYCCQYFTPTFG 120
|||
QY 121 GGTLEIKR 128
|||
Db      121 GGTKEIKR 129

RESULT 4
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig kappa chain V-II region CIL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorce J., Fong S., Heltmann J.G., Curo J.G., Chen P.P.,

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FT NON TER 1 1
 FT DISTLTD 26 86
 FT DISULFD 106 106
 FT VARIANT 83 83
 FT CONFLICT 14 14
 FT CONFLICT 57 57
 FT SEQUENCE 106 AA: 11609 MW: 51984DLPD37ACE8 CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 548; DB 1; Length 106;
 Matches 106; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
 Best Local Similarity 100.0%; Score 548; DB 1; Length 106;
 Matches 106; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TAAASVTFPPSPDEQKSTASVCLNNFYPREAKYOMKVDNALQSGNSDESYTEQDS 188
 DB 1 TAAASVTFPPSPDEQKSTASVCLNNFYPREAKYOMKVDNALQSGNSDESYTEQDS 188
 QY 189 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPTKSPNGEC 234
 DB 61 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPTKSPNGEC 234

RESULT 6
 KV3JL_HUMAN
 ID KV3JL_HUMAN STANDARD; PRT; 115 AA.

AC P04433: 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX MEDLINE-85087932; PubMed-6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus";
 RL Nucleic Acids Res. 12:9229-9236(1984).

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DR EMBL; X01668; NOT_ANNOTATED_CDS.
 DR PIR; A01900; K3HUV.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_V.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
 FT DOMAIN 21 >115
 FT DOMAIN 21 43
 FT DOMAIN 44 54
 FT DOMAIN 55 69
 FT DOMAIN 70 76
 FT DOMAIN 77 108
 FT DOMAIN 109 115
 FT DISULFD 43 108
 FT NON_TER 115 115
 FT SEQUENCE 115 AA: 12575 MW: 2DB4/CDA3A17D555 CRC64;

Query Match
 Best Local Similarity 45.0%; Score 545; DB 1; Length 115;
 Matches 107; Conservativity 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEAPQQLFLLLMLPDTGELVLTOSPATLSLSPERATLSCRASOSVSSYLAWYQKP 60
 DB 1 MEAPQQLFLLLMLPDTGELVLTOSPATLSLSPERATLSCRASOSVSSYLAWYQKP 60
 QY 61 GOAPRLITYDASNRATGIPRFGSGGSDFTLTISRLPEEDVALYCCOQYFTTP 115
 DB 61 GOAPRLITYDASNRATGIPRFGSGGSDFTLTISRLPEEDVALYCCOQYFTTP 115

RESULT 7
 KV3JL_HUMAN
 ID KV3JL_HUMAN STANDARD; PRT; 116 AA.

AC P04434: 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX MEDLINE-85087932; PubMed-6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus";
 RL Nucleic Acids Res. 12:9229-9236(1984).

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DR EMBL; X02725; NOT_ANNOTATED_CDS.
 DR PIR; A01901; K3HUV.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_V.
 DR SMART; SM00406; IGV_1.
 KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
 FT DOMAIN 21 >116
 FT DOMAIN 21 43
 FT DOMAIN 44 55
 FT DOMAIN 56 70
 FT DOMAIN 71 77
 FT DOMAIN 78 109
 FT DOMAIN 110 116
 FT DISULFD 43 109
 FT NON_TER 116 116
 FT SEQUENCE 116 AA: 12575 MW: 51CD55BA53B21929 CRC64;

Query Match
 Best Local Similarity 40.5%; Score 490.5; DB 1; Length 116;
 Matches 98; Conservativity 3; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEAPQQLFLLLMLPDTGELVLTOSPATLSLSPERATLSCRASOSVSSYLAWYQKP 59
 DB 1 MEAPQQLFLLLMLPDTGELVLTOSPATLSLSPERATLSCRASOSVSSYLAWYQKP 59
 QY 60 GOAPRLITYDASNRATGIPRFGSGGSDFTLTISRLPEEDVALYCCOQYFTTP 115
 DB 60 GOAPRLITYDASNRATGIPRFGSGGSDFTLTISRLPEEDVALYCCOQYFTTP 115

RESULT 8
 KV3JL_HUMAN

0Y 80 PRFSGSGTDTTTLTSLRLEPEDVALYCCQYFTTPTGCGSTRLEIKR 128
 Db 61 DFFSGSGTDTTTLTSLRLEPEDVALYCCQYFTTPTGCGSTRLEIKR 128
 RESULT 13
 K1W1_HUMAN
 ID K1W1_HUMAN STANDARD: PRF: 129 AA.
 AC P04431;
 DR 13-AUG-1987 (Rel. 05, Created)
 DE 15-JUL-1999 (Rel. 05, Last sequence update)
 OS Homo sapiens V-I region Walker precursor.
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.
 NCBI_TaxId=9606;
 RN 11
 RP
 SEQUENCE FROM N.A.
 RA MEDLINE=85014148; PubMed=6091049;
 RX Klobeck H.G., Combratio G., Zachau H.G.;
 RT Lymphoid cell lines are closely related.
 RL Nucleic Acids Res. 12:6995-7006(1984).
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 DR EMBL: X00965; CAJ25477.1; ALT_TERM.
 DR PIR: A01883; K1HMK.
 DR HSP: P01607; IRR.
 DR InterPro: IPR00306; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45 IG KAPPA CHAIN V-I REGION WALKER.
 FT DOMAIN 46 56 FRAMEWORK-1.
 FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 72 78 FRAMEWORK-2.
 FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 111 119 FRAMEWORK-3.
 FT DISULFID 120 129 COMPLEMENTARITY-DETERMINING-3.
 FT NON_TER 45 110 FRAMEWORK-4.
 FT 129 129 BY SIMILARITY.
 SQ
 129 AA: 14069 MW; F941PA07DAFCF9 CRC64;
 Query Match 36.68; Score 444; DB 1; Length 129;
 Best local 67.78; Pred. No. 66-31;
 Matches 86; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 0Y 1 MAPAPQLFLLLMLPTTGEIVLTOSPATLSLGERATSCRASQSVSYIANYQKP 60
 Db 3 MRVAPQLGLLLMLNGARCDIOMTQSPSLASVSGRVTITCRASQISNLNMYQKP 62
 61 GQAPRLIYASNRATGIPRPFSGSGTDTTTLTSLRLEPEDVALYCCQYFTTPTGCGSTRLEIKR 128
 Db 63 GKAPKLLIYASNSLQSGVTSRFSFGSGTDTTTLTSLRLEPEDVALYCCQYFTTPTGCGSTRLEIKR 128
 0Y 121 GTRLEIK 127
 Db 123 GTRLEIK 129

ID KVA4C_HUMAN STANDARD: PRT: 134 AA.
AC P06314;
DE 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
XX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=66041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: X02990; CAA26733.1;
DR PIR: A01905; K4H017.
DR HSP: P80362; IWTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Signal.
KW
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 92 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULEID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738B32 CRC64;
Query Match 36.5%; Score 442; DB 1; Length 134;
Best Local Similarity 61.9%; Pred. No. 9, 3e-31;
Matches 83; Conservative 22; Mismatches 23; Indels 6; Gaps 1;
DB 1 MEAPQQLFLLLMLPPTGEIVLTQSPATLSISGERATLSCRAQSV-----SSYL 54
1 NWLGQVVISLIMWISGAYGDIWVTSQSPDSLAVSLGERATINCKSSQSLIYSSDNKNTLA 60
QY 55 WTQKFGQAPRLIYDASNRATGIPPRSGSGSGTDFLTISRLEPEDVALYCCQYFTT 114
DB 61 WTQKFGQAPRLIYDASNRATGIPPRSGSGSGTDFLTISRLEPEDVALYCCQYFTT 120
QY 115 PYTFGQGTREIKR 128
DB 121 PYTFGQGTREIKR 134
RESULT 15
KV3F_HUMAN STANDARD: PRT: 109 AA.
ID KV3F_HUMAN
AC P01624;
DE 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
XX [1]
RN SEQUENCE
RP MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IgM anti-gamma globulins."
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC -1- GLOBULIN ACTIVITY.
DR PIR: A01897; K3H0PM.
DR HSP: P80362; IWTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region.
FT DISULEID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8AB86 CRC64;
Query Match 36.3%; Score 439.5; DB 1; Length 109;
Best Local Similarity 79.8%; Pred. No. 1, 2e-30;
Matches 87; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
DB 21 EIVLTQSPATLSISGERATLSCRAQSVS-SYLAWYQKFGQAPRLIYDASNRATGIP 79
1 EIVLTQSPATLSISGERATLSCRAQSVSINSYLAWYQKFGQAPRLIYDASNRATGIP 60
QY 80 PRSGSGSGTDFLTISRLEPEDVALYCCQYFTTPTFGQGTREIKR 128
DB 61 ARSGSGSGTDFLTISRLEPEDVALYCCQYFTTPTFGQGTREIKR 109

Search completed: April 23, 2003, 11:01:41
Job time: 14.9057.secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2003, 10:57:05 ; Search time 25.8934 Seconds
(without alignments)
1862.055 Million cell updates/sec

Title: US-09-806-276a-1
Perfect score: 1212
Sequence: 1 MEAPADLLFLLLMLPDTTG.....EVTGGLSPYTKSPNRGEC 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	961.5	79.3	239	4	Q8TCD0
2	752	62.0	238	11	Q99M37
3	737	60.8	238	11	Q8VC16
4	732	60.4	234	11	Q8VCP0
5	728	60.1	234	11	Q8R062
6	721	59.5	234	11	Q91WF8
7	719.5	59.4	233	11	Q8VC55
8	703	58.0	233	11	Q91WS9
9	699	57.7	235	11	Q91W12
10	698.5	57.6	235	11	Q91W12
11	665	54.9	234	11	Q8R028
12	479.5	39.6	109	4	Q9UL78
13	457.5	37.7	233	4	Q8TBC9
14	454	37.5	237	4	Q8UTV6
15	453.5	37.4	109	4	Q9UL86
16	452	37.3	237	4	Q8WUK4

17	446	36.8	108	4	Q9UL83	Q9UL83 homo sapien
18	432.5	35.7	109	4	Q9UL85	Q9UL85 homo sapien
19	410.5	33.9	236	4	Q96E61	Q96E61 homo sapien
20	407	33.6	108	4	Q9UL79	Q9UL79 homo sapien
21	405	33.4	108	4	Q9UL77	Q9UL77 homo sapien
22	398	32.8	108	4	Q9UL70	Q9UL70 homo sapien
23	397	32.7	233	4	Q96I69	Q96I69 homo sapien
24	396	32.6	235	11	Q99M11	Q99M11 mus musculu
25	395	32.6	116	4	Q96PF6	Q96PF6 homo sapien
26	390.5	32.2	107	4	Q96SA9	Q96SA9 homo sapien
27	385	32.1	240	4	Q8WTK3	Q8WTK3 mus musculu
28	380	31.4	238	11	Q9YF0	Q9YF0 mus musculu
29	378	31.2	111	11	Q92OE9	Q92OE9 mus musculu
30	375.5	31.0	106	5	Q94I10	Q94I10 schistosoma
31	375.5	31.0	134	11	Q8VDD0	Q8VDD0 mus musculu
32	366.5	30.2	109	4	Q9UL81	Q9UL81 mus musculu
33	361	29.8	109	11	Q92OE6	Q92OE6 mus musculu
34	360	29.7	108	11	Q8VJ10	Q8VJ10 mus musculu
35	355	29.3	107	11	Q9ER29	Q9ER29 mus musculu
36	353	29.1	127	11	Q92S59	Q92S59 mus musculu
37	347	28.6	99	11	Q9UL74	Q9UL74 mus musculu
38	341	28.1	114	4	Q9UL80	Q9UL80 mus sapien
39	332	27.4	103	11	Q9UL82	Q9UL82 mus musculu
40	329.5	27.2	104	11	Q9UL82	Q9UL82 mus musculu
41	329	27.1	101	11	Q9UL78	Q9UL78 mus musculu
42	327	27.0	107	11	Q9UL84	Q9UL84 mus musculu
43	322	26.6	97	11	Q9UL76	Q9UL76 mus musculu
44	303.5	25.0	241	11	Q92IA6	Q92IA6 mus musculu
45	284	23.4	109	6	Q9N0W5	Q9N0W5 oryctolagus

ALIGNMENTS

RESULT 1
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0: 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC022362; AAR22362.1;
KW Hypothetical protein 26234 MW: 26234 MW: FACHDC3A3B03871D CRC64;
SQ SEQUENCE 239 AA; 26234 MW: FACHDC3A3B03871D CRC64;

Query Match 79.3%; Score 961.5; DB 4; Length 239;
Best Local Similarity 76.6%; Pred. No. 5.8e-83;
Matches 183; Conservative 28; Mismatches 23; Indels 5; Gaps 1;

QY 1 MEAPADLLFLLLMLPDTTGRIYVOSPATISLPGERATLSCRASQV-----SSYLAW 55
1 KRLPQQLGLMLVPGSSGQVNTQSPSLPIYIGQPAISCRSQSLVYSDGNTYLMW 60
DB 1 KRLPQQLGLMLVPGSSGQVNTQSPSLPIYIGQPAISCRSQSLVYSDGNTYLMW 60
QY 56 YQKPGQAPRLIYDASNRATGIPRRFGSGSGTDFLTLSRLPEPDVYALYYCOQFTTP 115
61 FQARRGQSPRLIYKVSNRDSGVPDRFGSGSGTDFLTITRVEADVGVYFGQGTWHP 120
DB 61 FQARRGQSPRLIYKVSNRDSGVPDRFGSGSGTDFLTITRVEADVGVYFGQGTWHP 120
QY 116 YFPGGTLEIKRYAAASVFIFPPSDQLKSGTASVYVCLINNFYPREAKVQKVNALQ 175
121 STFGGGLTKLEIKRYAAASVFIFPPSDQLKSGTASVYVCLINNFYPREAKVQKVNALQ 180
DB 121 STFGGGLTKLEIKRYAAASVFIFPPSDQLKSGTASVYVCLINNFYPREAKVQKVNALQ 180
QY 176 SGNSESVTEQDSKDYSLSTLTLSKADYEKKRYACEVTHOGLSSPYTKSPNRGEC 234
SGNSESVTEQDSKDYSLSTLTLSKADYEKKRYACEVTHOGLSSPYTKSPNRGEC 234

Db 181 SGNSESVTEQDSKDYSLSTLTLKADYEKHYVACEVTHQGLSSPYTKSPNNGEC 238

RESULT 2

ID 099M37 PRELIMINARY; PRT; 238 AA.

AC 099M37; PRELIMINARY; PRT; 238 AA.

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE Hypothetical 26.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RE SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC02035; AAH02035.1; -

DR HSP; P01679; 2FBT

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003600; Ig_1ike.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00409; Ig_2.

DR SMART; SM00407; Ig_c1.

DR SMART; SM00406; IgV_1.

DR SMART; SM00410; Ig_1ike.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match Best Local Similarity 62.0%; Score 752; DB 11; Length 238;

Matches 139; Conservative 44; Mismatches 50; Indels 6; Gaps 2;

Db 1 MEAPQALLFLILMLPDTTGEIVLQSPATLSLSPGERATLSCRASQSV-----SSYLAW 55

1 MKLPVRL-VLMFWIPASSSDVVMOTPLSLPVSIGDQASISCRSSQSLVHNGNTYLHW 59

56 YQKPGQAPRLIYDASNRATGIPPRSGSGGTDFTLTSLRLEPEVVALYCCQYFTTP 115

60 YLQKPGQAPRLIYKVNRFSGVDFRSGSGGTDFTLTSLRLEPEVVALYCCQYFTTP 119

116 YTFGGGTLEIKRTVAASVFIPPSDQLKSGTASVYCLLNFPYPRKAVQKVDNALQ 175

120 YTFGGGTLEIKRTVAASVFIPPSDQLKSGTASVYCLLNFPYPRKAVQKVDNALQ 179

176 SGNSESVTEQDSKDYSLSTLTLKADYEKHYVACEVTHQGLSSPYTKSPNNGEC 234

180 QNGVLSWTDQDSKDYSLSTLTLKADYEKHYVACEVTHQGLSSPYTKSPNNGEC 238

RESULT 3

ID 08VC16 PRELIMINARY; PRT; 238 AA.

AC 08VC16; PRELIMINARY; PRT; 238 AA.

DT 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 21, Last annotation update)

DE Hypothetical 26.2 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RE SEQUENCE FROM N.A.

RA Strausberg R.;

Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC019760; AAH19760.1; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00409; Ig_2.

DR SMART; SM00407; Ig_c1.

DR SMART; SM00406; IgV_1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match

Best Local Similarity 60.8%; Score 737; DB 11; Length 238;

Matches 137; Conservative 45; Mismatches 51; Indels 6; Gaps 2;

Db 1 MEAPQALLFLILMLPDTTGEIVLQSPATLSLSPGERATLSCRASQSV-----SSYLAW 55

1 MKLPVRL-VLMFWIPASSSDVVMOTPLSLPVSIGDQASISCRSSQSLVHNGNTYLHW 59

56 YQKPGQAPRLIYDASNRATGIPPRSGSGGTDFTLTSLRLEPEVVALYCCQYFTTP 115

60 YLQKPGQAPRLIYKVNRFSGVDFRSGSGGTDFTLTSLRLEPEVVALYCCQYFTTP 119

116 YTFGGGTLEIKRTVAASVFIPPSDQLKSGTASVYCLLNFPYPRKAVQKVDNALQ 175

120 YTFGGGTLEIKRTVAASVFIPPSDQLKSGTASVYCLLNFPYPRKAVQKVDNALQ 179

176 SGNSESVTEQDSKDYSLSTLTLKADYEKHYVACEVTHQGLSSPYTKSPNNGEC 234

180 QNGVLSWTDQDSKDYSLSTLTLKADYEKHYVACEVTHQGLSSPYTKSPNNGEC 238

Query Match Best Local Similarity 60.4%; Score 732; DB 11; Length 234;

Matches 138; Conservative 35; Mismatches 61; Indels 0; Gaps 0;

Db 1 MEAPQALLFLILMLPDTTGEIVLQSPATLSLSPGERATLSCRASQSV-----SSYLAW 55

1 MSYPTQVIGLILCLTGACDILQTPSPASVSGEIVITTCASENIYISYLMWYQKQ 60

61 GQAPRLIYDASNRATGIPPRSGSGGTDFTLTSLRLEPEVVALYCCQYFTTP 120

```

DB 61 GKSPQLLYVNAKTLADGVSRFSGSSGTOFLKINSIDPDEGSGYCCQHSIPFTFGS 120
QY 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
DB 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
QY 181 ESYTEDOSKSTYSLSSTLTLSKADYEKKYVACEVTHQGLSSPYTKSFNRGEC 234
DB 181 NSWTDOSKSTYSMSSTLTLTKEDEYERHNSYTCATHTKSTSPYKSFNRNEC 234

```

RESULT 5

```

ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1;
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

```

```

Query Match 60.1%; Score 728; DB 11; Length 234;
Best Local Similarity 59.4%; Pred. No. 7e-61;
Matches 139; Conservative 34; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 1 MEAPQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAASQSVSYLAWYQOKP 60
DB 1 MMSAQFLGLLLCFQGTGRCIDIOFTTSSLSASIGDVRTISCRASQDISYLNWYQOKP 60
QY 61 GQAPRLIYDASNRAATGIPRPSGSGTDFLTLSRLEPDVALYCOQFTPTPTFGQ 120
DB 61 DGTAKLITRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 120
QY 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
DB 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
QY 181 ESYTEDOSKSTYSLSSTLTLSKADYEKKYVACEVTHQGLSSPYTKSFNRGEC 234
DB 181 NSWTDOSKSTYSMSSTLTLTKEDEYERHNSYTCATHTKSTSPYKSFNRNEC 234

```

RESULT 6

```

ID Q91MF8 PRELIMINARY; PRT; 234 AA.
AC Q91MF8;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1;
KW Interpro; IPR003006; Ig_MHC.

```

```

DR InterPro: IPR001865; Ribosomal_S2.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7912D2 CRC64;

```

```

Query Match 59.5%; Score 721; DB 11; Length 234;
Best Local Similarity 59.0%; Pred. No. 3.2e-60;
Matches 138; Conservative 34; Mismatches 62; Indels 0; Gaps 0;

```

```

QY 1 MEAPQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAASQSVSYLAWYQOKP 60
DB 1 MMSAQFLGLLLCFQGTGRCIDIOFTTSSLSASIGDVRTISCRASQDISYLNWYQOKP 60
QY 61 GQAPRLIYDASNRAATGIPRPSGSGTDFLTLSRLEPDVALYCOQFTPTPTFGQ 120
DB 61 DGTAKLITRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 120
QY 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
DB 121 GTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQSGNSQ 180
QY 181 ESYTEDOSKSTYSLSSTLTLSKADYEKKYVACEVTHQGLSSPYTKSFNRGEC 234
DB 181 NSWTDOSKSTYSMSSTLTLTKEDEYERHNSYTCATHTKSTSPYKSFNRNEC 234

```

RESULT 7

```

ID Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig.C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C37 CRC64;

```

```

Query Match 59.4%; Score 719.5; DB 11; Length 239;
Best Local Similarity 56.9%; Pred. No. 4.6e-60;
Matches 136; Conservative 43; Mismatches 55; Indels 5; Gaps 1;

```

```

QY 1 MEAPQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLSCRAASQSVSYLAWYQOKP 55
DB 1 MKPLVLLVLLVLLFTSPASSSDVVLTPVLSLVNIGQASISCKSKSLNSDGFYLLW 60
QY 56 YQKPGQAPRLIYDASNRAATGIPRPSGSGTDFLTLSRLEPDVALYCOQFTPTPT 115
DB 61 YLQKPGQAPRLIYDASNRAATGIPRPSGSGTDFLTLSRLEPDVALYCOQFTPTPT 120
QY 116 YTFGQTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQ 175
DB 121 YTFGQTRLEIKRTVAAPSVFIPEPDSQDLKSGTASVYCLNNFYPREAKVQKVDNALQ 180

```

QY 176 SGNSESVTEODSKDSTYSLSTLTLKADYEKHKVYACEVTHOGLSSPYTKSPNRCGC 234
 Db 181 QNGVLNMTWTDQDSKDSSTYSSMSTLTLTKDEYERHNSTYCEATHKTSPIVKSFNRRNC 239

RESULT 8

Q91WS9 PRELIMINARY; PRT; 233 AA.

AC Q91WS9; PRELIMINARY; PRT; 233 AA.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Hypothetical 25.8 kDa protein (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.

RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013496; AAH13496.1;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_2.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN.1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 58.0%; Score 703; DB 11; Length 233;
 Best Local Similarity 58.9%; Pred. No. 1.6e-58;

Matches 132; Conservative 35; Mismatches 57; Indels 0; Gaps 0;

QY 11 LLLMLPDTGEIYLTQSPATLSLSPERATLSGRASQSVSYLAHQPGAPRLIYD 70
 Db 10 LLLCPGSRDIDMTQTTSLSLASLDRTVYISGSGQGANIYMQKPDGIVKLITY 69
 QY 71 ASNRATGIPRESGSGSDFTLTIRLEPEDVALYCCOQYFTPTFGGRLKRTV 130
 Db 70 TSSLHSGVSRFSGSGSDYSLTISNLEPEDVATYCCOQYRLPWTFGGRLKIRAD 129
 QY 131 AASVTFPPSDQLKSGTAVYCLNNFYPREAKVQKVDNALQSGNSQVTEODSKD 190
 Db 130 AAPTYSIFPPSSQQLSGASVYCLNNFYPKDINVKMKIDSEKQNGVLNMTWTDQSKD 189
 QY 191 STYSLSTLTLKADYEKHKVYACEVTHOGLSSPYTKSPNRCGC 234
 Db 190 STYSSMSTLTLTKDEYERHNSTYCEATHKTSPIVKSFNRRNC 233

RESULT 9

Q91A5 PRELIMINARY; PRT; 214 AA.

AC Q91A5; PRELIMINARY; PRT; 214 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Kappa light chain of Mab7 (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.

RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv)."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132371; AAD40242.1;
 HSSP; P01679; 2FBJ.

DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IgV; 1.
 DR SMART; SM00410; Ig_Like; 1.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN.1.
 FT NON_TER
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 57.7%; Score 699; DB 11; Length 214;
 Best Local Similarity 59.3%; Pred. No. 3.4e-58;
 Matches 127; Conservative 37; Mismatches 50; Indels 0; Gaps 0;

QY 21 EYLTQSPATLSLSPERATLSGRASQSVSYLAHQPGAPRLIYDASNRATGIP 80
 Db 1 DIQLTQSPSSMYASIGERYITCKASODINSYLSWFOQKPKGKSPKTLIYRANRLVDGPS 60
 QY 81 RFGSGSGDTFTLTIRLEPEDVALYCCOQYFTPTFGGRLKRTVAAPSVFI 140
 Db 61 RFGSGSGDYSILTISLEPEDMGITYCQYDEFFTGSGTKLEIKRADAPVSI 120
 QY 141 SDEQLKSGTAVYCLNNFYPREAKVQKVDNALQSGNSQVTEODSKDSTYSLSTLT 200
 Db 121 SDEQLTSGASVYCLNNFYPKDINVKMKIDSEKQNGVLNMTWTDQDSKDSSTYSSMTLT 180
 QY 201 LSKADYEKHKVYACEVTHOGLSSPYTKSPNRCGC 234
 Db 181 LTKDEYERHNSTYCEATHKTSPIVKSFNRRNC 214

RESULT 10

Q91W12 PRELIMINARY; PRT; 235 AA.

AC Q91W12; PRELIMINARY; PRT; 235 AA.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Unknown (protein for MGC:6582).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC TISSUE=BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006643; AAH06643.1;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_2.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN.1.
 SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDBD5E8FEF CRC64;

Query Match 57.6%; Score 698.5; DB 11; Length 235;
 Best Local Similarity 60.9%; Pred. No. 4.4e-58;
 Matches 131; Conservative 31; Mismatches 52; Indels 1; Gaps 1;

QY 20 GEIYLTQSPATLSLSPERATLSGRASQSVSYLAHQPGAPRLIYDASNRATGIP 79
 Db 22 GQIVLTQSPALMSASPERVYTMTCSSASSV-SHHHWYQKSGTSPRMWIDPFKLTSGVP 80
 QY 80 RFGSGSGDTFTLTIRLEPEDVALYCCOQYFTPTFGGRLKRTVAAPSVFI 139
 Db 81 RFGSGSGDTFTLTIRLEPEDVALYCCOQYFTPTFGGRLKRTVAAPSVFI 140
 QY 140 PSDEQLKSGTAVYCLNNFYPREAKVQKVDNALQSGNSQVTEODSKDSTYSLSTLT 199
 Db 141 PSDEQLTSGASVYCLNNFYPKDINVKMKIDSEKQNGVLNMTWTDQDSKDSSTYSSMTLT 200
 QY 200 TLSKADYEKHKVYACEVTHOGLSSPYTKSPNRCGC 234

Db 201 TLTNDEYERHNSYTCENATHTSTSPYKSFNNREC 235

RESULT 11

Q8R028 PRELIMINARY; PRT; 234 AA.

AC Q8R028; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10990;

RP TISSUE=FROM N.A.

RA TISSUE=MAAMARY GLAND;

RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC028540; AAH28540.1; -

SO HYPOTHETICAL protein.

Query Match 234 AA; 25702 MW; 148377FC1CD0AER CRC64;

Best local Similarity 54.9%; Score 665; DB 11; Length 234;

Matches 127; Conservative 32; Mismatches 71; Indels 0; Gaps 0;

QY 5 AQLFLILMLPDTGEIYVTPSPATLSLSPGERATLSGRASQSVSYLAWYQKPGQAP 64

DB 5 APLSLILLCVDSRAETVYQSPASLSVATGEKVTIRICITSPDIDDMNMYQKPGEP 64

QY 65 RLITIDASNATGIPPRFSGSGGDTFTLTISRLPEEDVALYQCOQFTPTTGQSTR 124

DB 65 KLLISEGNTLRGVSRSSSGYGFTEITENTLSEVADYVYLOQSDNPELTFGAGTKL 124

QY 125 EIKRTVAAPSVYIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVNALQSGNSQSEVT 184

DB 125 ELKRDAAATVYIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVNALQSGNSQSEVT 184

QY 185 EODSDSTYSLSSTLTLSKADYKHYACVTHQGLSSPYTSFNNREC 234

DB 185 DODSKDSTYSMSSTLTTLTKDEYERHNSYTCENATHTSTSPYKSFNNREC 234

RESULT 12

Q9UL78 PRELIMINARY; PRT; 109 AA.

AC Q9UL78; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Myosin-reactive Immunoglobulin light chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP TISSUE=FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RT Young D.C.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.;

RT Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSSP; P80362; 1WTU.

DR InterPro; IPR003006; Ig_MHC.

DR Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP TISSUE=FROM N.A.

FT NON_TER 109 109

SO SEQUENCE 109 AA; 11646 MW; 5F675C32E7EE197 CRC64;

Query Match 39.6%; Score 479.5; DB 4; Length 109;

Best local Similarity 87.2%; Pred. No. 8e-38;

Matches 95; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLITLDASNRATGIP 79

DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLITLDASNRATGIP 60

QY 80 PRFSGSGGDTFTLTISRLPEEDVALYQCOQFTPTTGQSTRLEIKR 128

DB 61 DRFSGSGGDTFTLTISRLPEEDCAVYVYQCOYSSPLTFGGSTKVEIKR 109

RESULT 13

Q8TBC9 PRELIMINARY; PRT; 233 AA.

AC Q8TBC9; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Hypothetical 24.9 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP TISSUE=FROM N.A.

RA TISSUE=PRIMARY B-CELLS;

RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC022823; AAH22823.1; -

SO HYPOTHETICAL protein.

Query Match 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Best local Similarity 37.7%; Score 457.5; DB 4; Length 233;

Matches 101; Conservative 43; Mismatches 79; Indels 9; Gaps 6;

QY 7 LLLFLILMLPDTGEIYVTPSPATLSLSPGERATLSGRASQSVSYLAWYQKPGQAPRL 66

DB 6 LLLPLTLCTGSEASVETLQ-PPSVSVPGQFARITCSGDLKQYAYWYQKPGQAPVL 64

QY 67 LIYDASNATGIPPRFSGSGGDTFTLTISRLPEEDVALYQCOQFT--TPYTGQSTR 124

DB 65 VIYKDNERPSCGIPPRFSGSSGTTVLTISGVOAEDADYVYLOQSDNPELTFGAGTKL 124

QY 125 EI-KRTVAAPSVYIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVNALQSGNSQSE 182

DB 125 TVLGQPRAAASVYIFPPSDEQLKSGTASVYCLINNFYPREAKVQKVNALQSGNSQSE 182

QY 183 VTEODSKDSTYSLSSTLTLSKADYKHYACVTHQGLSSPYTSFNNREC 234

DB 183 TTTPSKQSNNTYASSTYLSLTFEQMKSHKSYSCQVYHEG--STVEKTVAVTEC 232

RESULT 14

Q8WTU6 PRELIMINARY; PRT; 237 AA.

AC Q8WTU6; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE Hypothetical 24.9 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP TISSUE=FROM N.A.

RA TISSUE=TONSIL;

FT Modified-site /note- "potential casein kinase II phosphorylation site"
 FT 209
 FT Modified-site /note- "potential casein kinase II phosphorylation site"
 FT 218
 FT Modified-site /note- "potential casein kinase II phosphorylation site"
 FT 223
 FT Binding-site /note- "potential casein kinase II phosphorylation site"
 FT 235..245
 FT /label- metal_binding_motif
 FT /note- "homologous to MSE55"
 FT 241
 FT Modified-site /note- "potential casein kinase II phosphorylation site"
 FT 241
 FT W0200020588-A2.
 FT
 FT 13-Apr-2000.
 FT
 FT 01-OCT-1999; 99WO-US22908.
 FT
 FT 02-OCT-1998; 98US-0165621.
 FT
 FT (INCY-) INCYTE PHARM INC.
 FT
 FT Tang YT, Corley NC, Guegler KU, Lu DAM;
 FT WPI: 2000-303775/26.
 FT N-PSDB; AAA09155.
 FT
 FT Purified polypeptide for treating or preventing disorders associated
 FT with decreased expression or activity of bone marrow-derived serum
 FT proteins
 FT
 FT Claim 1; Page 69; 72pp; English.
 FT
 FT Human bone marrow-derived serum proteins (BMDSP) 2 has chemical and
 FT structural similarity with MSE55. BMDSP-1 and BMDSP-2 are useful for
 FT treating or preventing a disorder associated with decreased expression
 FT or activity of BMDSP.
 FT Antagonists of BMDSP are useful for treating or preventing a disorder
 FT associated with increased expression or activity of bone marrow-derived
 FT serum proteins. The disorders include cancers (melanoma, adenocarcinoma,
 FT sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
 FT asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
 FT osteo, and rheumatoid arthritis), viral infections, parasitic infections
 FT (schistosoma, tapeworm), and vascular disorders (arteriosclerosis,
 FT hypertension, vasculitis).
 FT
 FT Sequence 254 AA;
 FT
 FT Query Match 100.0%; Score 1326; DB 21; Length 254;
 FT Best Local Similarity 100.0%; Pred. No. 1,5e-126;
 FT Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT
 FT 1 MPATPTLYLKANKKGGKFKLRDILSPDMSPPLSGPFRHTIHGKGQDVEGDISFLQ 60
 FT 1 MPATPTLYLKANKKGGKFKLRDILSPDMSPPLSGPFRHTIHGKGQDVEGDISFLQ 60
 FT
 FT 61 GNYELLPGNOKAHILGQFGPHNEFFRANSTSDSVFETPPSVLKNALSLPTIGSSQALML 120
 FT 61 GNYELLPGNOKAHILGQFGPHNEFFRANSTSDSVFETPPSVLKNALSLPTIGSSQALML 120
 FT
 FT 121 PLSPVTFNFKQESFGPAKLPRLSCEPVMERKAQEKSSLLNGTVHOGDTISWSSGASQ 180
 FT 121 PLSPVTFNFKQESFGPAKLPRLSCEPVMERKAQEKSSLLNGTVHOGDTISWSSGASQ 180
 FT
 FT 121 PLSPVTFNFKQESFGPAKLPRLSCEPVMERKAQEKSSLLNGTVHOGDTISWSSGASQ 180
 FT 121 PLSPVTFNFKQESFGPAKLPRLSCEPVMERKAQEKSSLLNGTVHOGDTISWSSGASQ 180
 FT
 FT 181 SSGORDSSSSLSFOYDMDPAEDMFDPPTPELILKTKTSPESSLDLTGSLSLQDLGP 240
 FT 181 SSGORDSSSSLSFOYDMDPAEDMFDPPTPELILKTKTSPESSLDLTGSLSLQDLGP 240
 FT
 FT 241 SLDEVLNVMDKNK 254
 FT 241 SLDEVLNVMDKNK 254
 FT
 FT 241 SLDEVLNVMDKNK 254
 FT 241 SLDEVLNVMDKNK 254

RESULT 2
 ABG25106
 ID ABG25106 standard; Protein; 538 AA.
 XX
 AC ABG25106;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #25097.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 XX
 DR N-PSDB; AAS89293.
 XX
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT
 PS Claim 20; SEQ ID NO 55465; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 538 AA;
 XX
 XX Query Match 42.4%; Score 562.5; DB 22; Length 538;
 XX Best Local Similarity 66.1%; Pred. No. 3e-48;
 XX Matches 115; Conservative 10; Mismatches 18; Indels 31; Gaps 2;
 XX
 XX 81 HNEFFRANSTSDSVFETPPSVLKNALSLPTIGSSQALMLPLSPVTFNFKQESFGPAKL 140
 XX 81 HNEFFRANSTSDSVFETPPSVLKNALSLPTIGSSQALMLPLSPVTFNFKQESFGPAKL 140
 XX
 XX 396 HHEFVLCN-----IKNVLPVAVRHG-----KESRPRAKL 424
 XX 396 HHEFVLCN-----IKNVLPVAVRHG-----KESRPRAKL 424
 XX
 XX 141 PRISCEPVMEERKAQEKSSLLNGTVHOGDTISWSSGASQSSGORDSSSSLSFOYDMDP 200
 XX 141 PRISCEPVMEERKAQEKSSLLNGTVHOGDTISWSSGASQSSGORDSSSSLSFOYDMDP 200

RESULT 5

AAM53373

ID AAM53373 standard; Protein; 137 AA.

XX AAM53373;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 25478.

XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer.

XX Homo sapiens.

XX WO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

XX Example 4; SEQ ID NO: 25478; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention.

XX Sequence 137 AA;

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DE Peptide #45 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human cervical epithelial cells -

XX Claim 27; SEQ ID NO 18437; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes

XX (SENP: see AAT10068-AAT28459). The present sequence is a peptide encoded

XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs

XX can be used to produce a single exon microarray, which can be used for

XX measuring human gene expression in a sample derived from human cervical

XX epithelial cells. By measuring gene expression, the probes are therefore

XX useful in grading and/or staging of diseases of the cervix, notably

XX cervical cancer.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 137 AA;

XX

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DE Peptide #45 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder.

XX Homo sapiens.

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XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 03-AUG-2000; 2000US-0608408.
XX PR 21-SEP-2000; 2000US-0632366.
XX PR 27-SEP-2000; 2000US-0234687.
XX PR 04-OCT-2000; 2000US-0236359.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488897/53.
XX DR WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID No 26277; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP;
XX CC see AAI13135-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders.
XX SQ Sequence 137 AA;

Query Match 19.3%; Score 256.5; DB 22; Length 137;
Best Local Similarity 53.8%; Pred. No. 5.6e-18;
Matches 56; Conservative 10; Mismatches 35; Indels 3; Gaps 2;

QY 1 MPAKPTIYKANNKKKKFKRLDILSPMISPLDGFRRHTIHGKEGQHDVFGDISFLQ 60
DB 35 MSTRKVPYLYK-RGSRKKRKKERLDLSSDMISPLDGFRRHTIHGSGGSDMGDISFLQ 93
QY 61 GNYELLPGNOEKA--HLGQFPGHNEFFRANSTSDSVFETPSPV 102
DB 94 GKFHLLPGTWEGPEDEGTFDLPFOFTRTATVCGRELPGPSPL 137

RESULT 8
AAM01361
ID AAM01361 standard; Protein; 137 AA.
XX AC AAM01361;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #43 encoded by probe for measuring human breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US00661.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.

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PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-476286/51.
XX DR WPI; 2001-476286/51.
XX PT Novel single exon nucleic acid probe used to measuring gene expression
XX PT in a human breast -
XX PS Claim 27; SEQ ID No 10101; 322pp; English.
XX CC The present invention relates to novel single exon nucleic acid probes
XX CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for measuring human gene expression in
XX CC a human breast sample, where the probe hybridises at high stringency to a
XX CC nucleic acid expressed in the human breast. The probes are useful for
XX CC predicting, diagnosing, grading, staging, monitoring and prognosing
XX CC diseases of the human breast, particularly those diseases with polygenic
XX CC aetiology. The diseases include: breast cancer, disorders of development,
XX CC inflammatory diseases of the breast, fibrocystic changes, proliferative
XX CC breast disease and non-carcinoma tumours.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 137 AA;

Query Match 19.3%; Score 256.5; DB 22; Length 137;
Best Local Similarity 53.8%; Pred. No. 5.6e-18;
Matches 56; Conservative 10; Mismatches 35; Indels 3; Gaps 2;

QY 1 MPAKPTIYKANNKKKKFKRLDILSPMISPLDGFRRHTIHGKEGQHDVFGDISFLQ 60
DB 35 MSTRKVPYLYK-RGSRKKRKKERLDLSSDMISPLDGFRRHTIHGSGGSDMGDISFLQ 93
QY 61 GNYELLPGNOEKA--HLGQFPGHNEFFRANSTSDSVFETPSPV 102
DB 94 GKFHLLPGTWEGPEDEGTFDLPFOFTRTATVCGRELPGPSPL 137

RESULT 9
ABG35381
ID ABG35381 standard; Peptide; 137 AA.
XX AC ABG35381;
XX DT 19-AUG-2002 (first entry)
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 25046.
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberculous scleriosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermani-Ky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX PD 15-NOV-2001.
XX PF 30-JAN-2001; 2001WO-US00665.
XX PR 04-FEB-2000; 2000US-180312P.

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PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 PS Claim 27; SEQ ID NO 25046; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagenen syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 137 AA:
 QY Query Match 19.3%; Score 256.5; DB 23; Length 137;
 DB Best Local Similarity 53.8%; Pred. No. 5.6e-18;
 DB Matches 56; Conservative 10; Mismatches 35; Indels 3; Gaps 2;
 QY 1 MPATPIYIKANKKKRFRKRLDLSPLDMSPLSGPFRTHHGKGGQDVYEDISFLQ 60
 DB 35 MSTVPIYILK-RGSRKKRKKELRLDLSPLSGPFRTHHGKGGQDVYEDISFLQ 93
 QY 61 GNYELPGNOKKA--HLGQFGHNEFFRANSTSDVFTETPSPY 102
 DB 94 GKPHLLGTWYEGPEDEGTDLPRQFTRTATVCGRELPPDPSPL 137

RESULT 10
 AAE01862
 ID AAE01862 standard; Protein; 349 AA.
 XX
 AC AAE01862;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mouse zmsel protein.
 XX
 KW Mouse; zmsel protein; Cdc42/Rac interactive binding protein; CRIB;
 KW Wiskott-Aldrich Syndrome; cancer; tumour; invasion; metastasis; asthma;
 KW digestion; actin polymerisation; cytoskeletal reorganisation; arthritis;
 KW testicular function; muscle inflammation; inflammatory bowel disease;
 KW diverticulitis; male infertility; male contraceptive agent; myocarditis;
 KW spermatogenesis; sperm capacitation; reperfusion ischaemia; psoriasis;
 KW melanoma; atherosclerosis; pelvic inflammatory disease; PID; eczema;
 KW scleroderma; cytosolic; vasotropic; dermatological; gene therapy.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Domain 1..145
 FT /note= "Conserved N-terminal domain"
 FT Domain 27..41
 FT /label= CRIB_motif
 FT Domain 146..329
 FT /note= "Variable C-terminal domain"
 FT Region 329..350
 FT /note= "Highly conserved C-terminal tail"
 XX
 PD MO200134803-A2.
 XX
 XX 17-MAY-2001.
 PF 09-NOV-2000; 2000MO-US30945.
 XX
 PR 10-NOV-1999; 99US-0438564.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Holloway JL, Gao Z, Whitmore TE;
 XX
 DR WPI: 2001-335928/35.
 DR N-PSDB: AAD05673.
 XX
 PT Novel human CRIB protein, zmsel and polynucleotide encoding the
 PT protein, for detecting human chromosomal abnormalities and for treating
 PT cancer, cardiovascular and inflammatory conditions -
 XX
 PS Claim 21; Fig 2; 132pp; English.
 XX
 CC The present invention relates to DNA and protein for zmsel, a novel
 CC human Cdc42/Rac interactive binding (CRIB) protein. CRIB proteins are
 CC implicated in human disease such as Wiskott-Aldrich Syndrome. Zmsel
 CC modulators are useful for modulating tumour cell motility, invasion and
 CC metastasis, gene transcription, contractility of various tissues, actin
 CC polymerisation and cytoskeletal reorganisation, digestion, testicular
 CC function and fertility. Zmsel sequence and its modulators are useful for
 CC treating cancer, inflammatory heart or cardiovascular conditions, muscle
 CC inflammation, inflammation during and after surgery, arthritis, asthma,
 CC inflammatory bowel diseases or diverticulitis, myocarditis, scleroderma,
 CC atherosclerosis, pelvic inflammatory disease (PID), eczema and other
 CC inflammatory diseases, male infertility or as male contraceptive agents
 CC and for modulating spermatogenesis and sperm capacitation. zmsel and
 CC anti-zmsel antibodies are useful in diagnosing inflammatory diseases,
 CC such as reperfusion ischaemia, psoriasis, arthritis, melanoma and other
 CC inflammatory diseases, male reproductive cancers such as prostate and
 CC testicular cancers. zmsel polynucleotide sequences are useful as probes
 CC or primers for detecting human chromosomal abnormalities. zmsel sequence
 CC is used in gene therapy. The present amino acid sequence is mouse
 CC zmsel protein.

Region	Variable C-terminal domain
FT	226..231
FT	/note="Variable C-terminal domain
FT	148..336
Domain	148..336

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/note= "Variable C-terminal domain"
226..231

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CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB057737-AB072072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1356 AA;

Query Match	9.8%;	Score 130.5;	DB 22;	Length 1356;
Best Local Similarity	24.3%;	Pred. No. 0.0013;		
Matches 63;	Conservative 34;	Mismatches 103;	Indels 59;	Gaps 13

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OY      1  MPAAKPIYLKAAKKKGGKFFRLITLSPDMISPLDGFERTIHKRGKGQDVPDFISFL- 59
Db      462  LPSSTRDSFSAVSDHRISKRLR-----TEMISKQDNFKTHGHGIDGA--TEDIADFLG 515
OY      60  -QGNTELLPGNOEKAKHLGQFPNGHNEFFRANSTSDSVETEP--SPYLKNAISLPTIGGS 115
Db      516  SSONNHP-----KQIATPYKPSEDI-EQTPLLPLPPTSPDSIQIATASG- 559
OY      116  QALMLPLSPVTFNS--KQSFQPAKLPRISCEPWEKAKQEKSSLLENGTV-----HQ 167
Db      560  -----YFPFGANSGGAMGTSNMPPTIPSAENTPKLIATNGOSSFDPASGSTEINPFPNRR 612
OY      168  GDTSWGSSGSAQSQSGDHSSSLSLSEQYDPWPAEDMFDPPTPELIIKGTAKSEESISDL 227
Db      613  GDDEL-EGFLHNYGADGKSVSHSET-----GW-----RPTSRKIVDDPHEHHEISDD- 657
OY      228  TGSILSLQIDIGPSILDEV 246
Db      658  --ETIADKLDFGSPSLDEI 674

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Search completed: April 23, 2003, 11:01:08
Job time : 56.6516 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 10:59:20 ; Search time 13.5328 seconds
(without alignments)
552.246 Million cell updates/sec

Title: US-09-806-276a-2

Perfect score: 1326
Sequence: 1 MEAKTPPIYKANNKRGKRF.....QLDGPSTLDEVLNMDKRNK 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: Issued Patents_AA:*
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfills1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	7.9	2332	1	US-07-864-004B-4
2	105	7.9	2332	1	US-08-251-937A-4
3	105	7.9	2332	1	US-08-212-133A-2
4	105	7.9	2332	1	US-08-276-594A-2
5	105	7.9	2332	1	US-08-474-503-2
6	105	7.9	2332	2	US-08-670-707A-2
7	105	7.9	2332	4	US-09-037-601-2
8	105	7.9	2332	4	US-09-324-867-3
9	105	7.9	2332	4	US-09-315-179-2
10	105	7.9	2332	4	US-09-523-656-2
11	105	7.9	2332	5	PCT-US93-03275-4
12	105	7.9	2332	5	PCT-US94-13200-2
13	105	7.9	2351	1	US-08-121-202-2
14	105	7.9	2351	1	US-08-366-851A-2
15	105	7.9	2351	6	5171844-2
16	105	7.9	2351	6	5422260-1
17	94	7.1	416	2	US-09-211-930-11
18	94	7.1	416	3	US-09-340-993-11
19	94	7.1	416	4	US-09-468-442-11
20	88	6.6	933	4	US-08-293-728-2
21	88	6.6	933	4	US-09-421-868-2
22	86	6.5	716	4	US-09-219-983A-20
23	86	6.5	1079	3	US-09-058-489-22
24	86	6.5	1142	2	US-08-993-118-7
25	86	6.5	1142	3	US-08-845-528C-7
26	86	6.5	1142	4	US-09-061-709-2
27	86	6.5	1240	3	US-09-058-489-23

28	86	6.5	1347	3	US-09-058-489-24	Sequence 24, Appl
29	85.5	6.4	966	1	US-08-571-758-2	Sequence 2, Appl1
30	85.5	6.4	966	1	US-08-909-984A-2	Sequence 2, Appl1
31	85.5	6.4	966	1	US-08-909-983-2	Sequence 2, Appl1
32	85	6.4	649	2	US-08-149-097D-37	Sequence 37, Appl
33	83.5	6.3	224	4	US-08-944-483-34	Sequence 34, Appl
34	83.5	6.3	462	3	US-08-875-944B-5	Sequence 5, Appl1
35	83.5	6.3	462	4	US-09-116-049-4	Sequence 4, Appl1
36	83.5	6.3	1037	4	US-09-428-711A-21	Sequence 21, Appl
37	83	6.3	478	1	US-08-127-499A-11	Sequence 11, Appl
38	83	6.3	478	1	US-08-482-847-11	Sequence 11, Appl
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40	83	6.3	512	4	US-09-124-900-2	Sequence 2, Appl1
41	83	6.3	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
42	82.5	6.2	1637	4	US-09-718-852-2	Sequence 2, Appl1
43	82.5	6.2	1637	4	US-09-718-852-2	Sequence 2, Appl1
44	82.5	6.2	1637	4	US-09-718-852-2	Sequence 2, Appl1
45	82	6.2	500	1	US-08-375-510-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-864-004B-4

; Sequence 4, Application US/07864004B

; Patent No. 5364771

; GENERAL INFORMATION:

; APPLICANT: Ioliar, John S.

; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Kilpatrick & Cody

; STREET: 1100 Peachtree Street

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: US

; ZIP: 30309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07864,004B

; FILING DATE: 07 APRIL 1992

; CLASSIFICATION: A35

; ATTORNEY/AGENT INFORMATION:

; NAME: Padst, Patricia L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: EMO106

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-815-6508

; TELEFAX: 404-815-6555

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2332 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapien

; TISSUE TYPE: Liver cDNA sequence

; US-07-864-004B-4

Query Match 7.9%; Score 105; DB 1; Length 2332;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPYIKAANKKKKKFKLDILSPDMIS-----PPLGDFRHTIHKEGOHVFGDISF- 58
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 799 TPHGLSLDLOAKYETSDSPGAIDSNNSLSMTFRQLH-----HS--GDMVFT 850
 QY 59 -----LQGNTELLPGNOEKAHLGQFPGHNEFFRANSTSDVFTETPSPVL-----KNAIS 108
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 851 PESGLQLRLNEKL--GTTAATELKLID-----FKVSTSNLILSTIPSDNLAACTDNTSS 903
 QY 109 LPTIGSQALMLPLSPVTPFNSKQES--FGPAKLPL--SCEPYMEKKAQEKSSILENGTV 165
 | : : : : : | : : : : : | : : : : : | : : : : :
 Db 904 LG-----PPMPVHDSQDLDTLFGKSSPLTESGGLPILSENNDSKLLSGLM 953
 QY 166 HOGDTSGWSSGSAQSS---QGRDSSSSLSSEQYPPDPAEDMFDPHTPCELIKGKTKSEE 222
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 Db 954 NSQESSGKNVSTESGRLFGKRAHGPALL-----TKDNALFKVSI SLKTKNTSN 1006
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RESULT 2

US-08-251-937A-4
 ; Sequence 4, Application US/08251937A

Patent No. 5583209
 ; GENERAL INFORMATION:

APPLICANT: Lollar, John S.
 APPLICANT: Runge, Marschall S.

TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
 NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kilpatrick & Cody

STREET: 1100 Peachtree Street
 CITY: Atlanta

STATE: Georgia
 COUNTRY: US

ZIP: 30309

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/251,937A
 FILING DATE: 31-MAY-1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Pratt, John S.

REGISTRATION NUMBER: 29,476
 REFERENCE/DOCKET NUMBER: EMU106DIV

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6367

TELEFAX: 404-815-6555
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids

TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein

HYPOTHETICAL: NO
 ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:

ORGANISM: Homo sapien
 TISSUE TYPE: Liver CDNA sequence

US-08-251-937A-4

Query Match

7.9%; Score 105; DB 1; Length 2332;

Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPYIKAANKKKKKFKLDILSPDMIS-----PPLGDFRHTIHKEGOHVFGDISF- 58
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 799 TPHGLSLDLOAKYETSDSPGAIDSNNSLSMTFRQLH-----HS--GDMVFT 850
 QY 59 -----LQGNTELLPGNOEKAHLGQFPGHNEFFRANSTSDVFTETPSPVL-----KNAIS 108
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 Db 851 PESGLQLRLNEKL--GTTAATELKLID-----FKVSTSNLILSTIPSDNLAACTDNTSS 903
 QY 109 LPTIGSQALMLPLSPVTPFNSKQES--FGPAKLPL--SCEPYMEKKAQEKSSILENGTV 165
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 Db 904 LG-----PPMPVHDSQDLDTLFGKSSPLTESGGLPILSENNDSKLLSGLM 953
 QY 166 HOGDTSGWSSGSAQSS---QGRDSSSSLSSEQYPPDPAEDMFDPHTPCELIKGKTKSEE 222
 :
 Db 954 NSQESSGKNVSTESGRLFGKRAHGPALL-----TKDNALFKVSI SLKTKNTSN 1006
 QY 223 SLSD---LTGSLSLDLDLGP SLDEVLN-----VMDKN 253
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 Db 1007 SATNRKTHIDGP--SLTIENSPVWONILSDTEFKKVTPLIHDMMLMDKN 1055

RESULT 3

US-08-212-133A-2
 ; Sequence 2, Application US/08212133A

Patent No. 5663060
 ; GENERAL INFORMATION:

APPLICANT: Lollar, John S.
 APPLICANT: Runge, Marschall S.

TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kilpatrick & Cody

STREET: 100 Peachtree Street
 CITY: Atlanta

STATE: Georgia
 COUNTRY: US

ZIP: 30303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/212,133A
 FILING DATE: March 11, 1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Fabst, Patrea L.

REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: EMU/76677

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-572-6508

TELEFAX: 404-572-6555
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids

TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein

HYPOTHETICAL: YES
 ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:

ORGANISM: Homo sapien
 TISSUE TYPE: Liver CDNA sequence

US-08-212-133A-2

Query Match

7.9%; Score 105; DB 1; Length 2332;

Query Match 7.9%; Score 105; DB 1; Length 2332;
 Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPVYKAANNKGGKFKRLDILSPDMIS-----PPLGDFRTHIIGREGQHDVFGDISF- 58
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 799 TPFGSLSDLOAKKETSDSPGALDSNNSLSMEHFRQLH-----HS--GDMVFT 850
 QY 59 -----LQGNTELLPGNOEKAHLGPPGHNEFFRANSTSDVFTETSPVY-----KNAIS 108
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 851 PESGQLRLNEMTL--GTTAATELRLKLD-----FKVSTSNMLISTIPSDNLAAGDTWSS 903
 QY 109 LPTIGGSQALMLPLSPVTFNSKQES--FGPAKLPR--SCEPVMEKQAEKSSILENGTV 165
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 904 LG-----PPSMVPIYHDSQDITLTFGKKSSPLTESGGPLSSENNDSKILLESGLM 953
 QY 166 HOGDTSGSSGSAOSS--QGRDSSSSLSRQYDPMFAEDMFHPTECELKIGKTKSEE 222
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 DB 954 NSQESSWGKNVSTESGRLFKGRRAHGPALL-----TKDNALFKVSI SLKTKTSNN 1006
 QY 223 SLSD-----LTGSLSLDLDLPSLIDEVLN-----VMDKN 253
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 1007 SATNRKTHIDG--SLIENSFVWONILLESDEFEKRYTPLIHDMMDKN 1055

RESULT 4
 US-08-276-594A-2
 ; Sequence 2, Application US/08276594A
 ; Patent No. 5693499

GENERAL INFORMATION:

APPLICANT: YONEMURA, Hiroshi
 APPLICANT: TAJIMA, Yoshitaka
 APPLICANT: SUGAMARA, Keishin
 APPLICANT: MASUDA, Kenichi
 TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
 TITLE OF INVENTION: FACTOR VIII PROTEIN COMPLEX
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/276,594A
 FILING DATE: 18-JUL-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/950,191
 FILING DATE: 24-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 243262/1991
 FILING DATE: 24-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 74129/195/AOPA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-276-594A-2

Query Match 7.9%; Score 105; DB 1; Length 2332;
 Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPVYKAANNKGGKFKRLDILSPDMIS-----PPLGDFRTHIIGREGQHDVFGDISF- 58
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 799 TPFGSLSDLOAKKETSDSPGALDSNNSLSMEHFRQLH-----HS--GDMVFT 850
 QY 59 -----LQGNTELLPGNOEKAHLGPPGHNEFFRANSTSDVFTETSPVY-----KNAIS 108
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 851 PESGQLRLNEMTL--GTTAATELRLKLD-----FKVSTSNMLISTIPSDNLAAGDTWSS 903
 QY 109 LPTIGGSQALMLPLSPVTFNSKQES--FGPAKLPR--SCEPVMEKQAEKSSILENGTV 165
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 904 LG-----PPSMVPIYHDSQDITLTFGKKSSPLTESGGPLSSENNDSKILLESGLM 953
 QY 166 HOGDTSGSSGSAOSS--QGRDSSSSLSRQYDPMFAEDMFHPTECELKIGKTKSEE 222
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 954 NSQESSWGKNVSTESGRLFKGRRAHGPALL-----TKDNALFKVSI SLKTKTSNN 1006
 QY 223 SLSD-----LTGSLSLDLDLPSLIDEVLN-----VMDKN 253
 || : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
 DB 1007 SATNRKTHIDG--SLIENSFVWONILLESDEFEKRYTPLIHDMMDKN 1055

RESULT 5
 US-08-474-503-2
 ; Sequence 2, Application US/08474503
 ; Patent No. 574446

GENERAL INFORMATION:

APPLICANT: Emory University
 APPLICANT: Hybrid Human/Animal Factor VIII
 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kilpatrick & Cody
 STREET: 1100 Peachtree Street, Suite 2800
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: US
 ZIP: 30309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,503
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Pratt, John S.
 REGISTRATION NUMBER: 29,476
 REFERENCE/DOCKET NUMBER: EMU106CIP(3)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6500
 TELEFAX: 404-815-6555
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapien
 TISSUE TYPE: Liver cDNA sequence
 US-08-474-503-2

Query Match 7.9%; Score 105; DB 1; Length 2332;
 Best Local Similarity 23.0%; Pred. No. 0.12; Mismatches 102; Indels 76; Gaps 15;
 Matches 67; Conservative 46;

QY 5 TPYIAANKKKKKFLRLDILSPDMIS-----PPLGDFRHTIIGKEGQHVFGDISF- 58
 DB 799 TPBGLSLSDLOEAKYETFDSPGALDSNLSSEMT HFRPOLH-----HS--GDMVFT 850
 QY 59 -----LOGNYELLPGNOEKAHLGPPGHNEFRANSTSDSVFTETPSPVL-----KNAIS 108
 DB 851 PESGLQRLNKL--GTTATELKLKD-----FKVSTSNMNLSTIPSDNLAAGTDWTS 903
 QY 109 LPTIGSQALMLPLSPYFNSKQES--FGPAKLPR--SCEPYMEKAEKSSILENGTV 165
 DB 904 LG-----PPSMVHYDSQDITLFGKKSPITSGGPLSISENNDSKLESGIM 953
 QY 166 HOGDTSMGSSGASOSS-----QGRDSHSSLSSEQYPDWPAEDMFDHPCELINGKTKSEE 222
 DB 954 NSQESSWGNVSTESGRLEFKGKRAHGPALL-----TKDNALFKVSIILKTKNTSNN 1006
 QY 223 SLSD-----LTGSLSLDLDLGPILDEVLN-----YMDKN 253
 DB 1007 SATNRKTHIDP--SLIENSPPVWQNLLESDTEFKKVTPLIHDMKMDKN 1055

RESULT 6

US-08-670-707A-2
 ; Sequence 2, Application US/08670707A
 ; Patent No. 5859204

GENERAL INFORMATION:

APPLICANT: Lollar, John S.
 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/670,707A
 FILING DATE: 26-JUN-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US94/13200
 FILING DATE: 15-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,133
 FILING DATE: 11-MAR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Greenlee, Lorraine L.
 REGISTRATION NUMBER: 27,894
 REFERENCE/DOCKET NUMBER: 75-95F
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/499-8089
 TELEFAX: 303/499-8089

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein

HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Liver
 US-08-670-707A-2

Query Match 7.9%; Score 105; DB 2; Length 2332;
 Best Local Similarity 23.0%; Pred. No. 0.12; Mismatches 102; Indels 76; Gaps 15;
 Matches 67; Conservative 46;

QY 5 TPYIAANKKKKKFLRLDILSPDMIS-----PPLGDFRHTIIGKEGQHVFGDISF- 58
 DB 799 TPBGLSLSDLOEAKYETFDSPGALDSNLSSEMT HFRPOLH-----HS--GDMVFT 850
 QY 59 -----LOGNYELLPGNOEKAHLGPPGHNEFRANSTSDSVFTETPSPVL-----KNAIS 108
 DB 851 PESGLQRLNKL--GTTATELKLKD-----FKVSTSNMNLSTIPSDNLAAGTDWTS 903
 QY 109 LPTIGSQALMLPLSPYFNSKQES--FGPAKLPR--SCEPYMEKAEKSSILENGTV 165
 DB 904 LG-----PPSMVHYDSQDITLFGKKSPITSGGPLSISENNDSKLESGIM 953
 QY 166 HOGDTSMGSSGASOSS-----QGRDSHSSLSSEQYPDWPAEDMFDHPCELINGKTKSEE 222
 DB 954 NSQESSWGNVSTESGRLEFKGKRAHGPALL-----TKDNALFKVSIILKTKNTSNN 1006
 QY 223 SLSD-----LTGSLSLDLDLGPILDEVLN-----YMDKN 253
 DB 1007 SATNRKTHIDP--SLIENSPPVWQNLLESDTEFKKVTPLIHDMKMDKN 1055

RESULT 7

US-09-037-601-2
 ; Sequence 2, Application US/09037601
 ; Patent No. 6180371

GENERAL INFORMATION:

APPLICANT: Lollar, John S.
 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/037,601
 FILING DATE: 26-JUN-1996
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US94/13200
 FILING DATE: 15-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,133
 FILING DATE: 11-MAR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fieber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER: 75-95F
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/499-8089
 TELEFAX: 303/499-8089

RESULT 10
 US-09-523-656-2
 ; Sequence 2, Application US/09523656
 ; Patent No. 6458563
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar S., John
 ; TITLE OF INVENTION: MODIFIED FACTOR VIII
 ; FILE REFERENCE: 75-951
 ; CURRENT APPLICATION NUMBER: US/09/523,656
 ; CURRENT FILING DATE: 2000-03-10
 ; EARLIER APPLICATION NUMBER: 09/037,601
 ; EARLIER FILING DATE: 1998-03-10
 ; EARLIER APPLICATION NUMBER: 08/670,707
 ; EARLIER FILING DATE: 1996-06-26
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 2332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-523-656-2

Query Match 7.9%; Score 105; DB 4; Length 2332;

Best Local Similarity 23.0%; Pred. No. 0.12; Indels 76; Gaps 15;

Matches 67; Conservative 46; Mismatches 102;

Qy 5 TPVYKAAANKKKKKRKLRLDILSPDMIS-----PPLGDFRRTIHIGKEGQHDVFGDISF- 58
 Db 799 TPVGLSLDLQAEKYEFTSDPSPGALDSNNSLSEMTFRPOLH-----HS--GDWFT 850
 Qy 59 -----LQGVYELLPGNOEKALHGFPGHNEFRANSTSDSVETETSPVL-----KNATIS 108
 Db 851 PEGSLQLRLNEKL--GTATATELKLID-----FKVSTSNLNLSTIPSDNLAACTDMTSS 903
 Qy 109 LPTIGSQALMLPLSPVTFNSKQES--FGPAKLPR-L-SCEPVMEKQAEKSSILENGTV 165
 Db 904 LG-----PPSMVHYDSQDITLFGKSSPLTESGGLPILSEENNDKILLESGLM 953
 Qy 166 HOGDTSGWSSGASOSS---OGRDSSSSLSSEQYPPWPAEDMFDHPPECLINKTKTSEE 222
 Db 954 NSQESSMGKVVSTESGRLEFKGRRAHGPALL-----TKDNALFKVSIISLTKTKTSNN 1006
 Qy 223 SLSD-----LTGSLSLDLQDLPGLDEVLN-----YMDKN 253
 Db 1007 SATNRKTHIDP--SLTIENSPVWQNLIESDTEFKKVTPLIHDMRLMDKN 1055

RESULT 11
 PCT-US93-03275-4
 ; Sequence 4, Application PC/TUS9303275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S.
 ; APPLICANT: Runge, Marschall S.
 ; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 1100 Peachtree Street, Suite 2800
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30309-4530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/03275
 ; FILING DATE: 19930407
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864004

FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: EMU 106PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-815-6508
 ; TELEFAX: 404-815-6555
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2332 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapien
 ; TISSUE TYPE: Liver cDNA sequence
 ; PCT-US93-03275-4

Query Match 7.9%; Score 105; DB 5; Length 2332;

Best Local Similarity 23.0%; Pred. No. 0.12;

Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

Qy 5 TPVYKAAANKKKKKRKLRLDILSPDMIS-----PPLGDFRRTIHIGKEGQHDVFGDISF- 58
 Db 799 TPVGLSLDLQAEKYEFTSDPSPGALDSNNSLSEMTFRPOLH-----HS--GDWFT 850
 Qy 59 -----LQGVYELLPGNOEKALHGFPGHNEFRANSTSDSVETETSPVL-----KNATIS 108
 Db 851 PEGSLQLRLNEKL--GTATATELKLID-----FKVSTSNLNLSTIPSDNLAACTDMTSS 903
 Qy 109 LPTIGSQALMLPLSPVTFNSKQES--FGPAKLPR-L-SCEPVMEKQAEKSSILENGTV 165
 Db 904 LG-----PPSMVHYDSQDITLFGKSSPLTESGGLPILSEENNDKILLESGLM 953
 Qy 166 HOGDTSGWSSGASOSS---OGRDSSSSLSSEQYPPWPAEDMFDHPPECLINKTKTSEE 222
 Db 954 NSQESSMGKVVSTESGRLEFKGRRAHGPALL-----TKDNALFKVSIISLTKTKTSNN 1006
 Qy 223 SLSD-----LTGSLSLDLQDLPGLDEVLN-----YMDKN 253
 Db 1007 SATNRKTHIDP--SLTIENSPVWQNLIESDTEFKKVTPLIHDMRLMDKN 1055

RESULT 12
 PCT-US94-13200-2
 ; Sequence 2, Application PC/TUS9413200
 ; GENERAL INFORMATION:
 ; APPLICANT: Emory University
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 1100 Peachtree Street, Suite 2800
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/13200
 ; FILING DATE: 15-NOV-1994
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: EMD106CIP(2)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6508
 TELEFAX: 404-815-6555
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapien
 TISSUE TYPE: Liver cDNA sequence
 PCT-US94-13200-2

Query Match 7.9%; Score 105; DB 5; Length 2332;
 Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

OY 5 TPYLKANKKKKKRKLIDILSPDMIS-----PPLGDFRHTIHGKGOHVFQDISF- 58
 DB 799 TPBGLSLDLOAKYETSPDPSGAIDSNLSLSEMTFRPOLH-----HS--GDWVFT 850
 OY 59 -----LQGNVELLPNGOEKALHGFPGHNEFFRANSTDSVFTETSPVL-----KNAIS 108
 DB 851 PPSGLQLRLNEKL--GTTATLTKLKD-----FKVSTSNMLISTIPSDNLAAGTDWTS 903
 OY 109 LPTIGSQALMLPLSPYTPNSKQES--FGPAKLPL--SCEPYMEKAKQESLLENGTV 165
 DB 904 LG-----PPSMVHYDSQDITLFGKSSPLTESGGPLSLENNDSKLLSGLM 953
 OY 166 HOGDTSWSSGASQSS---QGRSHSSSLSEQYDPWPAEDMFDPHPPCELIRKTRSEE 222
 DB 954 NQSESMGKNVSTESGRLEFKRAHGPALL-----TKDNALFKVSI SLKTKNTKNSN 1006
 OY 223 SLSD---LTSLSLSDLDLGP SLDEVLN-----VMDKN 253
 DB 1007 SATNKRTHIDGP--SLTIENSPVWQNTLESDETEFKKVTPLIHRLMDKN 1055

RESULT 13
 US-08-121-202-2
 Sequence 2, Application US/08121202
 Patent No. 5563045
 GENERAL INFORMATION:
 APPLICANT: Pittman, Debra
 APPLICANT: Rehmentulla, Alawaz
 APPLICANT: Wozney, John M.
 APPLICANT: Kaufman, Randal J.
 TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/121,202
 FILING DATE: 14-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Meinel, M. C.
 REGISTRATION NUMBER: 31,544
 REFERENCE/DOCKET NUMBER: GI 5195A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)876-1210 X8574
 TELEFAX: (617)876-5851
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2351 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-121-202-2

Query Match 7.9%; Score 105; DB 1; Length 2351;
 Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

OY 5 TPYLKANKKKKKRKLIDILSPDMIS-----PPLGDFRHTIHGKGOHVFQDISF- 58
 DB 818 TPBGLSLDLOAKYETSPDPSGAIDSNLSLSEMTFRPOLH-----HS--GDWVFT 869
 OY 59 -----LQGNVELLPNGOEKALHGFPGHNEFFRANSTDSVFTETSPVL-----KNAIS 108
 DB 870 PPSGLQLRLNEKL--GTTATLTKLKD-----FKVSTSNMLISTIPSDNLAAGTDWTS 922
 OY 109 LPTIGSQALMLPLSPYTPNSKQES--FGPAKLPL--SCEPYMEKAKQESLLENGTV 165
 DB 923 LG-----PPSMVHYDSQDITLFGKSSPLTESGGPLSLENNDSKLLSGLM 972
 OY 166 HOGDTSWSSGASQSS---QGRSHSSSLSEQYDPWPAEDMFDPHPPCELIRKTRSEE 222
 DB 973 NQSESMGKNVSTESGRLEFKRAHGPALL-----TKDNALFKVSI SLKTKNTKNSN 1025
 OY 223 SLSD---LTSLSLSDLDLGP SLDEVLN-----VMDKN 253
 DB 1026 SATNKRTHIDGP--SLTIENSPVWQNTLESDETEFKKVTPLIHRLMDKN 1074

RESULT 14
 US-08-366-851A-2
 Sequence 2, Application US/08366851A
 Patent No. 5681746
 GENERAL INFORMATION:
 APPLICANT: Bodner, Mordechai
 APPLICANT: De Polo, Nicolas J.
 APPLICANT: Hsu, David Chi-Tang
 APPLICANT: Chang, Steven
 TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Viagene, Inc.
 STREET: 11055 Roselle Street
 CITY: San Diego
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,851A
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Chambers, Daniel M.
 REGISTRATION NUMBER: 34,561
 REFERENCE/DOCKET NUMBER: 930049.438
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 452-1288
 TELEFAX: (619) 452-2616

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-366-851A-2

Query Match 7.9%; Score 105; DB 1; Length 2351;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPYLKANKKKGKFKRLDLSFDMIS-----PPLGDFRHTIHIGEGOHVFGDISF- 58
DB 818 TPHGSLSDQLEAKYEFSDPSGAIDSNLSSEMTHERPOLH-----HS--GDMVFT 869
QY 59 -----LQGWYELLPGNOEKALHGFPGHNEFFRANSTSDSVETETPSVYL-----KNAIS 108
DB 870 PEGSLQRLNEKL--GTTATELTKLD-----FKVSTSNLSTIPSDNLAGTDNTSS 922
QY 109 LPTIGSQALMLPLSPVTFNSKQES--FGPAKLPRL--SCEPYMEERKAQEKSSILENGTV 165
DB 923 LG-----PPSMVHYDSQDITLFGKSSPLTESGGLSLSENNDSKILBSGLM 972
QY 166 HOGDTSMGSSGASQSS---QGRDSHSSLSSEQYPPMPADMDPHPTPCELIKGKTSEE 222
DB 973 NSQESSMGKKNVSTESGRLEFKGRAGPALL-----TKDNALFKVYSISLTKNTKTSNN 1025
QY 223 SLSD---LFGSLSLQDLGPSLDEVLN-----VMDKN 253
DB 1026 SATNRKTHIDGP--SLIENSPVWONILSDTEFKKVTPLIHDRMLMDKN 1074

RESULT 15
5171844-2
; Patent No. 5171844
; APPLICANT: VAN COYEN, ALBERT J.J.; DANNEKOEK, HANS; VERBEET,
; MARTINDS P.; VAN LEEN, ROBERT W.
; TITLE OF INVENTION: PROTEINS WITH FACTOR VIII ACTIVITY
; PROCESS FOR THEIR PREPARATION USING GENETICALLY-ENGINEERED CELLS
; AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/205, 226
; FILING DATE: 10-JUN-1988
; SEQ ID NO: 2:
; LENGTH: 2351
5171844-2

Query Match 7.9%; Score 105; DB 6; Length 2351;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

QY 5 TPYLKANKKKGKFKRLDLSFDMIS-----PPLGDFRHTIHIGEGOHVFGDISF- 58
DB 818 TPHGSLSDQLEAKYEFSDPSGAIDSNLSSEMTHERPOLH-----HS--GDMVFT 869
QY 59 -----LQGWYELLPGNOEKALHGFPGHNEFFRANSTSDSVETETPSVYL-----KNAIS 108
DB 870 PEGSLQRLNEKL--GTTATELTKLD-----FKVSTSNLSTIPSDNLAGTDNTSS 922
QY 109 LPTIGSQALMLPLSPVTFNSKQES--FGPAKLPRL--SCEPYMEERKAQEKSSILENGTV 165
DB 923 LG-----PPSMVHYDSQDITLFGKSSPLTESGGLSLSENNDSKILBSGLM 972
QY 166 HOGDTSMGSSGASQSS---QGRDSHSSLSSEQYPPMPADMDPHPTPCELIKGKTSEE 222
DB 973 NSQESSMGKKNVSTESGRLEFKGRAGPALL-----TKDNALFKVYSISLTKNTKTSNN 1025
QY 223 SLSD---LFGSLSLQDLGPSLDEVLN-----VMDKN 253
DB 1026 SATNRKTHIDGP--SLIENSPVWONILSDTEFKKVTPLIHDRMLMDKN 1074

Search completed: April 23, 2003, 11:04:02
Job time : 23.5328 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 11:01:15 ; Search time 15.6148 Seconds

(Without alignments)
1303.445 Million cell updates/sec

Title: US-09-806-276a-2

Sequence: 1 MPAAPIYIKAAANNKGRK.....QLDLPSTLDEVLYNMDKNK 254

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Gapop 10.0, Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB_PEP:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_PEP:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_PEP:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_PEP:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_PEP:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_PEP:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256.5	19.3	137	10	US-09-864-761-42650
2	109.5	8.3	938	9	US-10-029-217A-28
3	109.5	8.3	938	9	US-10-029-217A-28
4	105	7.9	2332	9	US-09-957-641-2
5	105	7.9	2332	9	US-10-187-319-2
6	105	7.9	2332	9	US-10-187-319-2
7	104	7.8	2344	10	US-09-815-242-12713
8	92	6.9	560	9	US-09-815-242-13057
9	88.5	6.7	1239	9	US-09-291-417-13
10	88	6.6	936	1	US-08-781-986A-5249
11	87	6.6	371	9	US-09-925-299-806
12	86	6.5	271	10	US-09-925-299-806
13	86	6.5	473	10	US-09-864-761-38321
14	86	6.5	525	10	US-09-817-676A-12
15	86	6.5	617	10	US-09-817-676A-12
16	86	6.5	1031	10	US-09-815-242-10932
17	86	6.5	1142	9	US-10-085-108-7
18	86	6.5	1142	10	US-09-899-651-2

20	86	6.5	1175	10	US-09-771-161A-224	Sequence 224, App
21	86	6.5	1175	10	US-09-771-161A-225	Sequence 225, App
22	86	6.5	1175	10	US-09-771-161A-226	Sequence 226, App
23	86	6.5	1702	9	US-09-854-133-434	Sequence 434, App
24	86	6.5	1702	10	US-09-738-973-434	Sequence 435, App
25	85.5	6.4	741	9	US-09-738-626-4455	Sequence 4455, App
26	85.5	6.4	1237	9	US-10-108-605-211	Sequence 211, App
27	85.5	6.4	1394	9	US-10-108-605-211	Sequence 213, App
28	85.5	6.4	3256	10	US-09-919-172-98	Sequence 98, App
29	85	6.4	588	10	US-09-820-905-4	Sequence 2, App11
30	85	6.4	589	10	US-09-820-905-4	Sequence 4, App11
31	84	6.3	606	10	US-09-820-905-5	Sequence 5, App11
32	84	6.3	1002	9	US-09-988-117-5	Sequence 3, App11
33	84	6.3	1002	10	US-09-812-471-3	Sequence 3, App11
34	84	6.3	1002	10	US-09-812-633-3	Sequence 3, App11
35	84	6.3	1350	9	US-09-952-060-35	Sequence 35, App1
36	83.5	6.3	247	10	US-09-923-779-154	Sequence 154, App
37	83.5	6.3	462	9	US-09-884-363-4	Sequence 4, App11
38	83	6.3	363	9	US-10-003-035-37	Sequence 37, App1
39	83	6.3	453	9	US-10-003-035-39	Sequence 39, App1
40	83	6.3	599	9	US-10-003-035-39	Sequence 59, App1
41	83	6.3	764	9	US-10-081-119-30	Sequence 30, App1
42	82.5	6.2	227	10	US-09-864-761-36295	Sequence 36295, A
43	82.5	6.2	276	10	US-09-864-761-38306	Sequence 38306, A
44	82	6.2	1021	10	US-09-815-242-5471	Sequence 5471, App
45	82	6.2	1021	10	US-09-815-242-12544	Sequence 12544, A

ALIGNMENTS

RESULT 1
US-09-864-761-42650
Sequence 42650, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 42650
 LENGTH: 137
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC000353.21
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.62
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 39
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
 OTHER INFORMATION: SWISSPROT HIT: Q00587, EVALUATE 3.00e-07
 OTHER INFORMATION: EST_HUMAN HIT: BF058866.1, EVALUATE 4.00e-76
 OTHER INFORMATION: EST_HUMAN HIT: T75138.1, EVALUATE 3.00e-60
 US-09-864-761-42650

Query Match 19.3%; Score 256.5; DB 10; Length 137;
 Best Local Similarity 53.8%; Pred. No. 3.2e-16;
 Matches 56; Conservative 10; Mismatches 35; Indels 3; Gaps 2;
 Oy 1 MPKPTIYKANKKRRKRLDILSPDMISPLDGFRTTHIGKQGVDFGDISFLQ 60
 Db 35 MSTVPIYIK-RGSRKRGKRLDILSDMISPLDGFRTTHIGKQGVDFGDISFLQ 93
 Oy 61 GVEYLLPGNOEKA-HLGQFPGHNEFRANSTDSVTEPPSPY 102
 Db 94 GKEFLLPGMVGEPEDEGTFDLPGQFRTATVCGRELPLDPSFL 137

RESULT 2
 US-10-029-217A-28
 Sequence 28, Application US/10029217A
 Patent No. US20020164735A1
 GENERAL INFORMATION:
 APPLICANT: OLSON, ERIC N.
 APPLICANT: WANG, DA-ZHI
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
 FILE REFERENCE: US/10/029,217A
 CURRENT APPLICATION NUMBER: US/10/029,217A
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 60/257,761
 PRIOR FILING DATE: 2000-12-21
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 28
 LENGTH: 938
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-029-217A-28

Query Match 8.3%; Score 109.5; DB 9; Length 938;
 Best Local Similarity 24.2%; Pred. No. 0.14;
 Matches 81; Conservative 31; Mismatches 106; Indels 117; Gaps 17;
 Oy 2 PAKPTIYKANKKGG-----KKFKRLDILSPDM--ISPLDGFRT 40
 Db 227 PPTPIAVHAHVSKSLGDSKNRRHKRPDPKPKYKIKLTIQYIPPOKAKKSPPPMD5AY 286
 Oy 41 THIGKEGQHDVFGDISFLQNTYELLPGNOEK-----AHLGQFPGHNEFRANSTS 91

Db 287 ARLLQOOO-----LFLQ--LQILSQOOOQOQHRFSYLGMMHQALKEPNCQVWNPNS 336
 Oy 92 DSV-FTEPPSYLKNKAIIS-----LPTIGSSQA 117
 Db 337 SSTPLSNTPLSPVKNSSFGQGVSSFKPGPLPMLDLKVELKQOLRIKGLVSGTKTA 396
 Oy 118 LMLPL-----LSPTFNSKQESFPAKLPRLSCEPVEKKAQKESLLE 161
 Db 397 LMDRLRPFQDCSGNPVPNFGDITVTF-----PVTNPLPNY-----QSSSTALS 443
 Oy 162 NGTVHQDTSWSSGSSASOSQGRDSSSSLSQYIPDMPADMD-HPTECELKTKTS 220
 Db 444 NGFYHFGSTS--SSPPISSASDL-SVAGSLPDTEND--ASPSGLHPSPVHVC-----T 493
 Oy 221 EESL-SDTLGSLSLQDLGLPSLDEVLNVMQNK 254
 Db 494 EESLMSLNGSVSPSLDGLDSEKDKML--VEROK 526

RESULT 3
 US-10-029-217A-29
 Sequence 29, Application US/10029217A
 Patent No. US20020164735A1
 GENERAL INFORMATION:
 APPLICANT: OLSON, ERIC N.
 APPLICANT: WANG, DA-ZHI
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
 FILE REFERENCE: US/10/029,217A
 CURRENT APPLICATION NUMBER: US/10/029,217A
 PRIOR FILING DATE: 2002-03-19
 PRIOR APPLICATION NUMBER: 60/257,761
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 29
 LENGTH: 938
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-029-217A-29

Query Match 8.3%; Score 109.5; DB 9; Length 938;
 Best Local Similarity 24.2%; Pred. No. 0.14; 106; Indels 117; Gaps 17;
 Matches 81; Conservative 31; Mismatches 106; Indels 117; Gaps 17;
 Oy 2 PAKPTIYKANKKGG-----KKFKRLDILSPDM--ISPLDGFRT 40
 Db 227 PPTPIAVHAHVSKSLGDSKNRRHKRPDPKPKYKIKLTIQYIPPOKAKKSPPPMD5AY 286
 Oy 41 THIGKEGQHDVFGDISFLQNTYELLPGNOEK-----AHLGQFPGHNEFRANSTS 91
 Db 287 ARLLQOOO-----LFLQ--LQILSQOOOQOQHRFSYLGMMHQALKEPNCQVWNPNS 336
 Oy 92 DSV-FTEPPSYLKNKAIIS-----LPTIGSSQA 117
 Db 337 SSTPLSNTPLSPVKNSSFGQGVSSFKPGPLPMLDLKVELKQOLRIKGLVSGTKTA 396
 Oy 118 LMLPL-----LSPTFNSKQESFPAKLPRLSCEPVEKKAQKESLLE 161
 Db 397 LMDRLRPFQDCSGNPVPNFGDITVTF-----PVTNPLPNY-----QSSSTALS 443
 Oy 162 NGTVHQDTSWSSGSSASOSQGRDSSSSLSQYIPDMPADMD-HPTECELKTKTS 220
 Db 444 NGFYHFGSTS--SSPPISSASDL-SVAGSLPDTEND--ASPSGLHPSPVHVC-----T 493
 Oy 221 EESL-SDTLGSLSLQDLGLPSLDEVLNVMQNK 254
 Db 494 EESLMSLNGSVSPSLDGLDSEKDKML--VEROK 526
 RESULT 4
 US-09-957-641-2

Sequence 2, Application US/0957641
Publication No. US20020182670A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-00
CURRENT APPLICATION NUMBER: US/09/957,644
CURRENT FILING DATE: 2001-09-16
PRIOR APPLICATION NUMBER: US 60/234047
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: US 60/236460
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2332
TYPE: PRT
ORGANISM: Homo sapiens
US-09-957-641-2

Query Match	7.9%	Score 105;	DB 9;	Length 2332;
Best Local Similarity	23.0%	Pred. No. 1.3;		
Matches 67;	Conservative 46;	Mismatches 102;	Indels 76;	Gaps 15

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OY      5  TPYTKAANKKKKKFKFRLDILSPDMIS-----PPLGDGRRHTIHIGKEGQHVDFDSE  58
Db      799  TPHGLSLSDLOAEKYETFFSDPSPGALDSNNLSSETHTRPOLH-----HS-GDMVFT  850

OY      59  -----LOGNETLLPGNOEKAHLGQEPHNEFRANSTSDSVYETTPSPVL---KNAIS  108
Db      851  PESGIQRLINKEKT--GTTAATELKLID-----FKVSTSNNNLITSPSNNLAACTDNSS  903

OY      109  LPTTGGSCAALMLPLLSVYENSKOES--FGAPALPBL--SCEPYMEBKAQEKSLLENGTV  165
Db      904  LG-----PSPMVHYHDSQDITLTKKSSPLTESGGPGLSSENNDSKLLSGLM  953

OY      166  HQGDTSMGSSGGSASQSS--QGNDSSHSSLSSEQYPMWPAEDMFDAHPCELIKGTAKSEE  222
Db      954  NSQSSMOKNIVSTESGRLETKRAKHAPALL-----TKDNALFKVSTLSLTKTKTSNN  1006

OY      223  SLSD-----LNGSLSLSDLDLGPSLDLYVLN-----YMKXN  253
Db      1007  SATNKCTHIDP--SLTIENSPWONITSDTEFKKVTPLIDRLMKLN  1055

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RESULT 5
US-10-187-319-2
; Sequence 2, Application US/10187319
; Publication No. US20030068785A1

APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SOURCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 3370 Mannattan Circle Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,319
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601

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1      FILING DATE: 1998-03-10
2      APPLICATION NUMBER: WO PCT/US97/111555
3      FILING DATE: 1997-06-26
4      APPLICATION NUMBER: US 08/670,707
5      FILING DATE: 1996-06-26
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Greenlee, Lorraine L.
8      REGISTRATION NUMBER: 27,894
9      REFERENCE/DOCKET NUMBER: 75-95K
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 303/499-8080
12     TELEFAX: 303/499-8089
13     INFORMATION FOR SEQ ID NO: 2:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 2332 amino acids
16     TYPE: amino acid
17     STRANDEDNESS: single
18     TOPOLOGY: <unknown>
19     MOLECULE TYPE: protein
20     HYPOTHEetical: YES
21     ANTI-SENSE: NO
22     FRAGMENT TYPE: N-terminal
23     ORIGINAL SOURCE:
24     ORGANISM: Homo sapiens
25     TISSUE TYPE: Liver
26     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
27
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;	SEQUENCE DESCRIPTION:	SEQ ID NO:	2:
US-10-187-319-2			

Query Match: 7.98; Score 105; DB 9; Length 2332;

Best Local Similarity 23.0%; Pred. No. 1.3;
Matches 67; Conservative 46; Mismatches 102; Indels 76; Gaps 15;

[illegible]

RESULT 6
US-10-132-829-4
; Sequence 4, Application US/10132829
; Publication No. US20030044982A1

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/  APPLICANT: Hoshijima, Masahiko
/
/  TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor
/
/  TITLE OF INVENTION: with vesicle vector
/
/  FILE REFERENCE: 6627-Pa1170
/
/  CURRENT APPLICATION NUMBER: US/10/132,829
/
/  CURRENT FILING DATE: 2002-04-25
/
/  PRIOR APPLICATION NUMBER: 60/286,314
/
/  PRIOR FILING DATE: 2001-04-25
/
/  NUMBER OF SEQ ID NOS: 5
/
/  SOFTWARE: PatentIn version 3.1
/
/  SEQ ID NO 4
/
/  LENGTH: 2351
/
/  TYPE: PRT
/
/  ORGANISM: Homo sapiens
/

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[illegible]

US-08-/81-986A-5249
; Sequence 5249, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION.

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 525
CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ENTRY DATE:

FILED DATE: 11/11/2011
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert

REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: DB34881

TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5249:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5249

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Query Match	6.6%	Score 88;	DB 1;	Length 936;
Best Local Similarity	21.7%	Pred. No. 13;		
Matches 57;	Conservative 25;	Mismatches 121;		

[illegible]

Db 380 KKGKFNLSIKETIQIDIKTNNTYRQRTIYVPSDSNYI---APVLTGN--LKPNTDSNAL 43
 Oy 75 L60-----

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Db
435 IDQNTSIKVKYVDNADI,SESYEVNDENEDYVNCUUT-----EPGHNEEFFRANSTSDSVETE 97
      :|               ||::|||

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98 TPSPVLKNAISLPITIGSQALMLPLL-----SDVENSCKOTATGCTA--
QY

Db 494 TPPIVVNGHIDPNSKGLALRSTLYGVNSNIIRMSMWDEVAEFNNSSGSDGIDVNNY EF
GFVINSKQESFGPAKPLRL 14

144 SCEPMEKAEKSSILENGTVHOGDTWSSGASQSSOGRDSSHSSLSLEQYPDWPAED 20

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554 ---PEQPDGEIEPIPIPDSDSDPGSDSGSDSNDSGSDSGSDSTSDSGSDASDSAS 61

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204 MEDHPTPCELIKGKTSEESLSD 226
      | : :
611 ----- : : | |
      D-----

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011 USUSASDSDSASDSDSASDSDSD 633

RESULT 11
IS-09-533-029-110

Sequence 110, Application US/09533029
Publication No. US20030046723A1

GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Brown, J.

APPLICANT: Brown, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddle, James

APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc

APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James

APPLICANT: Yu, Guo-Liang
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver

APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne

TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010

CURRENT APPLICATION NUMBER: US/09/533, 029
 CURRENT FILING DATE: 2000-03-22
 PUBLISHED DATE: 2000-03-22

EARLIER FILING DATE: 1999-03-23
 NUMBER OF SEQ. TD NOS.: 101
 EARLIER APPLICATION NUMBER: 60/125,814
 EARLIER INVENTOR:

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110

LENGTH: 371
TYPE: PRT

ORGANISM: *Arabidopsis thaliana*
FEATURE:

ORGAN INFORMATION: G1650
-09-533-029-110

Query Match	6.68;	Score 87;	DB 9;	Length 371;
Best Local Similarity	26.48;	Pred no	4;	

Matches	Conservative	Mismatches	Indels	Gaps
63;	30;	94;	52;	52;

Wed Apr 23 13:51:13 2003

us-09-806-276a-2.rapb

Page 6

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Db 126 PPRAGIILADPRTGTHILAEKRAENFNISQRCNI-----FLGGEAVDPS 171
QY 88 NSTSDSVETETSPVYKNAISLPTIGG--SQALMLPLSP-----VTFSKQSFSPAKL 140
Db 172 NSTLLSATES-IPATHTESRATYTGVSRTFPAVGLGPKGKVALEIAGTQSGW---L 227
QY 141 PRLSCEPVMEKQKESLLENGTVHOGDTWSGSSASQSGRDHSS-----S 191
Db 228 CKAETEVOKAPTEETDIDDERKRTRETNYENOG---TEENADTSSKRSRAIMRK 283
QY 192 LSEQYDPWAEFDFHPTCELIKTKTSEES--LSDLTGSLSLDLDLGPGLDEVYN 248
Db 284 LSERRRQKINEMW--KALQELLPRCTKTRDSMLDVTYKSLQ-----SQIADVLN 335

RESULT 12
US-09-925-299-806
; Sequence 806, Application US/09925299
; Publication No. US2003040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 806
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-806

Query Match
Best Local Similarity 24.2%; Pred. No. 3.7; Indels 52; Gaps 8;
Matches 48; Conservative 21; Mismatches 77;

QY 28 PDMTSPPLG-----DFRHT-----IHGEGQHDVFGDIS-----FLGNYEL 65
Db 73 PDVTEPPGPDNCLHFNMTPCQYRPOSVPBPHNKLQHOVYGANSEPPASGLRYNTYV 132
QY 66 LFGNDEKHAHQPGPHNEFRANST--DSVETETSPVYKNAISLPTIGSQALMLPL 123
Db 133 AGRNASHGHSKPCSRVEYVSSLSVYRNTCYPDIDP-----YPTIRYQSLHAPS 185
QY 124 S-----PYTFNSKQSFSPAKLPRLSCEPVMEKQKES-----LLENGTVH 166
Db 186 SMIRSPVISRTEVPDDEPAYCPR---PLYQYKPYQSSQARSQDYHTQLOPYFENGRAV 241
QY 167 QGDTWSGSSGASQSSOG 184
Db 242 YRSPYSSSSSTYSPPDG 259

RESULT 13
US-09-925-299-806
; Sequence 806, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
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QY 28 PDMTSPPLG-----DFRHT-----IHGEGQHDVFGDIS-----FLGNYEL 65
Db 73 PDVTEPPGPDNCLHFNMTPCQYRPOSVPBPHNKLQHOVYGANSEPPASGLRYNTYV 132
QY 66 LFGNDEKHAHQPGPHNEFRANST--DSVETETSPVYKNAISLPTIGSQALMLPL 123
Db 133 AGRNASHGHSKPCSRVEYVSSLSVYRNTCYPDIDP-----YPTIRYQSLHAPS 185
QY 124 S-----PYTFNSKQSFSPAKLPRLSCEPVMEKQKES-----LLENGTVH 166
Db 186 SMIRSPVISRTEVPDDEPAYCPR---PLYQYKPYQSSQARSQDYHTQLOPYFENGRAV 241
QY 167 QGDTWSGSSGASQSSOG 184
Db 242 YRSPYSSSSSTYSPPDG 259

RESULT 14
US-09-864-761-38321
; Sequence 38321, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aegomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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QY 28 PDMTSPPLG-----DFRHT-----IHGEGQHDVFGDIS-----FLGNYEL 65
Db 73 PDVTEPPGPDNCLHFNMTPCQYRPOSVPBPHNKLQHOVYGANSEPPASGLRYNTYV 132
QY 66 LFGNDEKHAHQPGPHNEFRANST--DSVETETSPVYKNAISLPTIGSQALMLPL 123
Db 133 AGRNASHGHSKPCSRVEYVSSLSVYRNTCYPDIDP-----YPTIRYQSLHAPS 185
QY 124 S-----PYTFNSKQSFSPAKLPRLSCEPVMEKQKES-----LLENGTVH 166
Db 186 SMIRSPVISRTEVPDDEPAYCPR---PLYQYKPYQSSQARSQDYHTQLOPYFENGRAV 241
QY 167 QGDTWSGSSGASQSSOG 184
Db 242 YRSPYSSSSSTYSPPDG 259

Query Match
Best Local Similarity 24.2%; Pred. No. 3.7; Indels 52; Gaps 8;
Matches 48; Conservative 21; Mismatches 77;

QY 28 PDMTSPPLG-----DFRHT-----IHGEGQHDVFGDIS-----FLGNYEL 65
Db 73 PDVTEPPGPDNCLHFNMTPCQYRPOSVPBPHNKLQHOVYGANSEPPASGLRYNTYV 132
QY 66 LFGNDEKHAHQPGPHNEFRANST--DSVETETSPVYKNAISLPTIGSQALMLPL 123
Db 133 AGRNASHGHSKPCSRVEYVSSLSVYRNTCYPDIDP-----YPTIRYQSLHAPS 185
QY 124 S-----PYTFNSKQSFSPAKLPRLSCEPVMEKQKES-----LLENGTVH 166
Db 186 SMIRSPVISRTEVPDDEPAYCPR---PLYQYKPYQSSQARSQDYHTQLOPYFENGRAV 241
QY 167 QGDTWSGSSGASQSSOG 184
Db 242 YRSPYSSSSSTYSPPDG 259

PRIORITY FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 806
LENGTH: 271
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-806
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 38321
;; LENGTH: 473
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
;; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUE 2.00e-48
;; OTHER INFORMATION: EST_HUMAN HIT: BB895761.1, EVALUE 4.00e-71
US-09-864-761-38321
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Query Match 6.5%; Score 86; DB 10; Length 473;
Best Local Similarity 23.9%; Pred. No. 8;
Matches 62; Conservative 24; Mismatches 73; Indels 100; Gaps 13;
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QY 32 SPLLGFRRTHIGK---EQCHD-----VFQDISFLQGN 62
DB 34 SPEGQVQSLHSPQSPPEGMHQSPLQSPESAPAGEDSLPQIPQSPLEGEDSLSLH 93
QY 63 YELLPGNOEKA---HLGPPGHNEFFR-----ANSTDSV---FTEPPSPVLKN 105
DB 94 FPQSPPEWEDSLPLHPQPPQGEDPQSLQSPVATCSSTSLSLPQSPESPQOS---- 149
QY 106 AISLPTIGSQALMLPLLSPT-----FNSKQES---FGPAKLPRLSCEPVME 150
DB 150 ----PPEGPAQS---PLQRRVSSFFSYTLASLLQSSHESQSPPEGPAQSPLOS--PVSS 200
QY 151 EKAQEKSSLLNGTVHOGDTSMGSSSSASQSSSGGRDSSSSLSSEQYPPDPAEDMFDHPPT 210
DB 201 FPSSTSSSLQSSSPV-----SSFPSTSSSLSSKSSPESPLOQ-----SP 238
QY 211 CELIKGKTK-----SEESLS 225
DB 239 VISFSSSTSLSPFSEBSS 257
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RESULT 15
US-09-814-550-2
;; Sequence 2, Application US/09814550
;; Patent No. US20020102641A1
;; GENERAL INFORMATION:
;; APPLICANT: Schlavi, Susan
;; APPLICANT: Madden, Stephen
;; APPLICANT: Manavalan, Parthasarathy
;; APPLICANT: Levine, Michael
;; APPLICANT: Jan de Beur, Suzanne
;; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
;; FILE REFERENCE: 501AUS
;; CURRENT APPLICATION NUMBER: US/09/814,550
;; CURRENT FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 60/191,786
;; PRIOR FILING DATE: 2000-03-24
;; PRIOR APPLICATION NUMBER: US 60/241,598
;; PRIOR FILING DATE: 2000-10-19
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 525
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;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-814-550-2
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Query Match 6.5%; Score 86; DB 10; Length 525;
Best Local Similarity 22.8%; Pred. No. 9.2;
Matches 44; Conservative 26; Mismatches 73; Indels 50; Gaps 8;
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QY 47 EGOHVFGDISFLQGNVETLPGNQ-----EKAHLQF-----PGHNEFFRANSTSDS 93
DB 336 EGSNDIMST-----NFKELPREGNRYDAGSQNHHQGVFHYHPAPASKERKREGSSDA 390
QY 94 V----FTEPP-----SPVKNATSLPTIGSQALMLPLLS-PVTENSK 131
DB 391 AESTYWNTEIPKNGKSTRGVDHNSNRQATLNKQRFPSKSGQLPIPSRGIDNEIKNE 450
QY 132 QESF-GPAKLPRLSCEPVMEKAQEKSSLLNGTVHOGDTSMG-----SSGSASQ 181
DB 451 MDSPNGPSHENITTHRGVHYVPHRQNNSTRNKGPQKSGWGRQPHSNRRFSSRRRDS 510
QY 182 SGRDSSSSLSLE 194
DB 511 SSSSDSGSSSED 523
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Search completed: April 23, 2003, 11:04:32
Job time : 19.6148 secs
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